

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:40:47 ; Search time 141.143 Seconds  
(without alignments)  
43.582 Million cell updates/sec

Title: US-10-067-484-1  
Perfect score: 62  
Sequence: 1 XXSGISNTVYANPK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

A\_Geneseq\_21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1980s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	14	5	AB881968
2	39	62.9	106	2	AAW88497
3	39	62.9	106	3	AAW88497
4	39	62.9	120	8	ADJ37083
5	39	62.9	329	7	ADC94153
6	39	62.9	401	4	ABR06884
7	39	62.9	474	4	AAU04831
8	39	62.9	489	6	ABP99325
9	39	62.9	490	6	ABU13218
10	39	62.9	493	6	ABP99326
11	39	62.9	637	7	ABO62726
12	39	62.9	673	8	ADR88952
13	39	62.9	858	2	AAK30477
14	39	62.9	1024	2	AAW19604
15	39	62.9	1522	8	ADN20818
16	38	61.3	120	4	AAO65232
17	38	61.3	329	6	ABO00477
18	38	61.3	336	6	ABU49299
19	38	61.3	432	3	AAAB18414
20	38	61.3	432	3	AAAB18414
21	38	61.3	433	4	AAW40128
22	38	61.3	440	3	AAAB43115
23	38	61.3	505	4	AAW41914
24	38	61.3	552	8	AD541744

25	38	61.3	560	8	ABO85007
26	38	61.3	602	2	ABG02902
27	38	61.3	705	8	ABO85006
28	38	61.3	1851	4	AAU00023
29	38	61.3	1851	5	AAO17860
30	38	59.7	138	5	ABP11408
31	37	59.7	219	4	AAAB63630
32	37	59.7	268	4	AAAB63629
33	37	59.7	376	6	ABG72091
34	37	59.7	389	3	AAW75076
35	37	59.7	389	3	AAW75077
36	37	59.7	389	3	AAW75078
37	37	59.7	399	3	ABE65138
38	37	59.7	441	6	ABP78454
39	37	59.7	515	6	ADC95690
40	37	59.7	586	6	ABJ26507
41	37	59.7	586	6	ABJ25907
42	37	59.7	700	4	AAAG83279
43	37	59.7	700	5	ABE94250
44	37	59.7	712	2	AAK06471
45	37	59.7	712	2	AAW33359
46	37	59.7	712	2	AAW49853
47	37	59.7	712	2	AAW80485
48	37	59.7	712	2	AAW49327
49	37	59.7	712	8	ADT98484
50	37	59.7	731	4	AAAB48573
51	37	59.7	829	6	AAO29907
52	37	59.7	830	6	ABU15713
53	37	59.7	831	6	ABU41378
54	37	59.7	841	7	ABO84388
55	37	59.7	975	7	AAE37942
56	37	59.7	1012	9	ADK06539
57	37	59.7	1012	9	ADY15120
58	37	59.7	1197	8	ADG66805
59	37	59.7	1343	4	ADU33259
60	37	59.7	1397	7	ADD42761
61	37	59.7	1430	4	ABBS8602
62	37	59.7	1751	5	ABG91039
63	37	59.7	1751	5	ABB94292
64	37	59.7	1751	5	ABB94371
65	37	59.7	1751	7	ADD43820
66	37	59.7	1751	9	ADW29022
67	37	59.7	1751	9	AEA19112
68	37	59.7	1752	3	AAAB1637
69	37	59.7	1752	3	AAAG83205
70	37	59.7	1752	5	ABB94176
71	36	58.1	201	4	AAW17341
72	36	58.1	201	4	ABB36350
73	36	58.1	201	4	AAW29848
74	36	58.1	201	4	ABB31155
75	36	58.1	201	4	ABB21708
76	36	58.1	201	4	AAW69509
77	36	58.1	201	4	AAW57117
78	36	58.1	201	4	ABG51183
79	36	58.1	201	4	AAW05030
80	36	58.1	201	5	ABG39134
81	36	58.1	243	6	ABP78956
82	36	58.1	261	4	AAW41917
83	36	58.1	281	8	ADT07818
84	36	58.1	287	7	ADG96570
85	36	58.1	297	7	ADC95679
86	36	58.1	303	4	AAW40131
87	36	58.1	303	4	AAE10992
88	36	58.1	303	5	AAAG78490
89	36	58.1	303	7	ADCT1018
90	36	58.1	303	7	AAE39894
91	36	58.1	303	7	ADP42456
92	36	58.1	303	8	ADQ48425
93	36	58.1	370	6	ABU20944
94	36	58.1	376	8	ADY77082
95	36	58.1	389	8	ADY09869
96	36	58.1	444	8	ADH12847
97	36	58.1	461	2	AAV34463

ABO85007	Human can
ABG02902	Novel hum
ABO85006	Murine ca
AAU00023	Human act
AAO17860	Pyrim dom
ABP11408	Human ORF
AAAB63630	Human gas
AAAB63629	Human gas
ABG72091	P1romycas
AAW75076	Neisseria
AAW75077	Neisseria
AAW75078	Neisseria
ABE65138	Drosophila
ABP78454	N. gonorr
ADC95690	E. faeciu
ABJ26507	Aspergill
ABJ25907	Aspergill
AAAG83279	Chlamydia
ABE94250	Chlamydia
AAK06471	Derived p
AAW33359	Human isl
AAW49853	Human pan
AAW80485	Islet cel
AAW49327	Pancreat
ADT98484	Human bre
AAAB48573	Human org
AAO29907	Human org
ABU15713	Protein e
ABU41378	Protein e
ABO84388	Pseudomon
AAE37942	Human CGD
ADK06539	Cyclin-de
ADY15120	PRO polyp
ADG66805	Novel hum
ADU33259	Novel hum
ADD42761	Chlamydia
ABBS8602	Drosophila
ABG91039	Chlamydia
ABB94292	Chlamydia
ABB94371	Chlamydia
ADD43820	Chlamydia
ADW29022	C. trachom
AEA19112	Chlamydia
AAAB1637	C. tracho
AAAG83205	Protein e
ABB94176	Chlamydia
AAW17341	Peptide #
ABB36350	Peptide #
AAW29848	Peptide #
ABB31155	Peptide #
ABB21708	Protein #
AAW69509	Human bon
AAW57117	Human bra
ABG51183	Human liv
AAW05030	Peptide #
ABG39134	Human pep
ABP78956	N. gonorr
AAW41917	Human pol
ADT07818	Plant ful
ADG96570	Human hea
ADC95679	E. faeciu
AAW40131	Human lip
AAE10992	Human lip
AAAG78490	50090 hum
ADCT1018	Human NOV
AAE39894	Human hyd
ADP42456	Human ppi
ADQ48425	Human hyd
ABU20944	Protein e
ADY77082	Plant ful
ADY09869	Plant ful
ADH12847	Francisel
AAV34463	Porphyrom

98	36	58.1	462	AAVY4339	AY434339 Porphyrom
99	36	58.1	466	ABU00023	ABu40023 Proteinn e
100	36	58.1	468	ABU16641	ABu16641 Proteinn e
101	36	58.1	533	ABU27821	ABu27821 Proteinn e
102	36	58.1	683	ADXS5021	ADxs5021 Plant ful
103	36	58.1	832	ABBS2141	ABbs2141 Drosophil
104	36	58.1	976	ABU03087	ABu03087 Amino amy
105	36	58.1	976	ADU07388	ADu07388 Amino aci
106	36	58.1	1016	AAAP94035	AAp94035 Delta-end
107	36	58.1	1180	AAAP82589	AAp82589 Insectici
108	36	58.1	1180	AAAP93715	AAp93715 Delta-end
109	36	58.1	1180	AAAP14373	AAp14373 Dipteran
110	36	58.1	1180	ADAP89426	ADp89426 cry4Aa.1
111	36	58.1	1180	ADAP83078	ADp83078 B.c. toxi
112	36	58.1	1194	AAAB917825	AAb917825 Chlamydia
113	35.5	57.3	981	ABAB91507	ABb91507 Herbicida
114	35.5	57.3	1224	ABAP23448	ABp23448 Bacterial
115	35	56.5	52	ABAP33084	ABp33084 Human tra
116	35	56.5	97	ABAP75438	ABp75438 Human sec
117	35	56.5	159	ADAP86365	ADp86365 Enterococ
118	35	56.5	284	ADLO5438	ADl05438 M.-catatr
119	35	56.5	302	ADH010412	ADh010412 Myb-relat
120	35	56.5	311	ADH050108	ADh50108 Soybean M
121	35	56.5	311	ADAB08586	ADa08586 Allidococ
122	35	56.5	315	ADBN26009	ADbn26009 Bacterial
123	35	56.5	343	ADBA48067	ADb48067 listeria
124	35	56.5	417	ADXY9755	ADx9755 Plant ful
125	35	56.5	417	ADXY15828	ADx15828 Hydroxyph
126	35	56.5	442	ADRO00550	ADr00550 Drosocin ca
127	35	56.5	453	ABU21443	ABu21443 Proteinn e
128	35	56.5	455	ADBF08003	ADf08003 Bacterial
129	35	56.5	456	ABBS5584	ABb5584 Lactococcc
130	35	56.5	468	ABBA91648	ABb91648 M. xanthu
131	35	56.5	610	ABBB6385	ABb6385 Drosophil
132	35	56.5	713	ADU07872	ADu07872 Amino aci
133	35	56.5	767	ADU43801	ADu43801 Human pro
134	35	56.5	867	ADBU41082	ADb41082 Proteinn e
135	35	56.5	870	ADFO4463	ADf04463 Bacterial
136	35	56.5	928	ADDS24039	ADd24039 Bacterial
137	35	56.5	1400	ABBS5412	ABb5412 Human phi
138	35	56.5	1545	ADAP09345	ADa09345 Helicobac
139	35	56.5	1545	ADAP61675	ADa61675 Bacteri
140	35	56.5	1602	ADBJ15212	ADb15212 Bacteri
141	35	56.5	2223	ADU912136	ADu912136 Haemophil
142	35	56.5	2223	ADCP98324	ADc98324 HEp-1
143	34.5	52.6	1623	ADSC20020	ADs20020 Bacteri
144	34	54.8	40	ADBA58857	ADb58857 Human car
145	34	54.8	40	ADU21889	ADu21889 Human car
146	34	54.8	40	ADU07275	ADu07275 Human car
147	34	54.8	40	ADU50509	ADu50509 P-optimib
148	34	54.8	74	ABMS1578	ABm1578 Peptide #
149	34	54.8	74	ABAM1074	ABa1074 Peptide #
150	34	54.8	98	ABBS2967	ABbs2967 Proteinn #
151	34	54.8	98	ABBS2480	ABbs2480 Human liv
152	34	54.8	98	ABBS4860	ABbs4860 Human liv
153	34	54.8	123	ABBS8783	ABbs8783 L. pneumo
154	34	54.8	123	ABBA1979	ABb1979 L. pneumo
155	34	54.8	222	ABBB7573	ABb7573 Mouse rib
156	34	54.8	225	ABAR04723	ABa04723 Sequence
157	34	54.8	232	ADBS06522	ADb06522 staphyloc
158	34	54.8	232	ADBS06088	ADb06088 staphyloc
159	34	54.8	234	AAAG06725	AAg06725 Arabidops
160	34	54.8	234	AAAG04390	AAg04390 Arabidops
161	34	54.8	238	ADTS6806	ADt56806 Plant pol
162	34	54.8	244	ADFO7302	ADf07302 Bacterial
163	3				

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:12 ; Search time 12.8571 Seconds  
(without alignments)  
104.765 Million cell updates/sec

Title: US-10-067-484-1

Perfect score: 62  
Sequence: 1 XXSGISNTVYANPK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	41	66.1	382	2	E83846 D-alanyl-D-alanine
2	39	62.9	673	2	T47905 hypothetical prote
3	39	62.9	1024	2	C64208 oligopeptidase ABC t
4	38	61.3	336	2	F82242 hypothetical prote
5	37	59.7	93	2	D69262 hypothetical prote
6	37	59.7	339	2	E84671 penicillin-binding
7	37	59.7	389	2	H81146 probable serine-ly
8	37	59.7	389	2	D81875 pyruvate kinase, p
9	37	59.7	562	2	S44287 organic solvent to
10	37	59.7	653	2	F70383 conserved hypothet
11	37	59.7	830	2	E83031 hypothetical prote
12	37	59.7	1751	2	G71518 hypothetical prote
13	36	58.1	117	2	C64378 restriction endonu
14	36	58.1	205	2	AC3366 type II restrictio
15	36	58.1	243	2	S43887 phosphoglycerate m
16	36	58.1	507	2	F81130 paraaporal crystal
17	36	58.1	243	2	E64247 hypothetical prote
18	36	58.1	969	2	T15446 hypothetical prote
19	36	58.1	1180	2	A26858 paraaporal crystal
20	36	58.1	1180	2	I39870 hypothetical prote
21	35.5	57.3	981	2	C96712 hypothetical prote
22	35	56.5	225	2	A97735 arabinose operon r
23	35	56.5	310	2	AB0275 N-acetylglutamate
24	35	56.5	343	2	AG1273 N-acetylglutamate
25	35	56.5	343	2	AH1636 probable 4-hydroxy
26	35	56.5	442	2	T14353 hypothetical prote
27	35	56.5	456	2	E86903 glutamine syntheta
28	35	56.5	469	2	AC2794 glutamine syntheta
29	35	56.5	469	2	B97573

30	35	56.5	469	2	AB3374
31	35	56.5	572	2	S75141
32	35	56.5	473	2	S55982 asparagine synthas
33	35	56.5	591	2	A99444 acylaminoacyl-pept
34	35	56.5	657	2	T24605 hypothetical prote
35	35	56.5	716	2	AB6181 hypothetical prote
36	35	56.5	939	2	AE2275 Iga-specific metal
37	35	56.5	1545	2	B41859 hypothetical prote
38	35	56.5	1802	2	G71616 fatty-acyl-CoA sym
39	34.5	55.6	2076	2	S15999 hypothetical prote
40	34	54.8	72	2	G97134 unknown protein f
41	34	54.8	75	2	AB6487 hypothetical prote
42	34	54.8	131	2	G72653 hypothetical prote
43	34	54.8	169	2	E97775 probable 2-oxoglut
44	34	54.8	227	2	T06362 hypothetical prote
45	34	54.8	263	2	AB2069 oxidase like prote
46	34	54.8	342	2	S57814 hypothetical prote
47	34	54.8	342	2	H84898 penicillin-binding
48	34	54.8	389	2	AH3003 conserved hypothet
49	34	54.8	398	2	A99280 ATP-dependent RNA
50	34	54.8	408	2	S66705 dipeptidase (impor
51	34	54.8	423	2	A96450 glutamate-ammonia
52	34	54.8	443	2	AB2872 hypothetical prote
53	34	54.8	474	2	F86819 hypothetical prote
54	34	54.8	476	2	F81340 H+-exporting ATPas
55	34	54.8	479	2	T02623 hypothetical prote
56	34	54.8	481	2	G86144 carboxypeptidase C
57	34	54.8	485	2	S37050 fibronectin-bindin
58	34	54.8	495	2	B85964 oligopeptide ABC t
59	34	54.8	495	2	C91119 oligopeptide ABC t
60	34	54.8	512	2	T41340 glucose oxidase (B
61	34	54.8	518	2	E87754 probable PPE prote
62	34	54.8	532	1	CPBYV hypothetical prote
63	34	54.8	550	2	B97346 NAD-dependent mal
64	34	54.8	570	2	B97160 isoguinoline 1-oxi
65	34	54.8	594	2	D64676 ubiquitin-specific
66	34	54.8	595	2	D71841 G protein-coupled
67	34	54.8	605	1	A35459 hypothetical prote
68	34	54.8	645	2	F70825 unknown protein f
69	34	54.8	704	2	S76120 glutamate synthase
70	34	54.8	766	2	C87689 probable PPE prote
71	34	54.8	781	2	B56939 phenazine biosynth
72	34	54.8	875	2	T50182 jacalin beta-1 cha
73	34	54.8	961	2	S67568 hypothetical prote
74	34	54.8	962	2	JC5808 probable regulator
75	34	54.8	1286	1	S38058 probable murein ge
76	34	54.8	1286	1	A96616 glutathione transf
77	34	54.8	3097	2	T28635 probable ribosomal
78	34	54.8	3300	2	D70575 basophilic protein
79	34	54.8	3472	2	T31308 NADH2 dehydrogenas
80	33.5	54.0	290	2	AF3234 sfah protein precu
81	33	53.2	20	2	S29636 yb1s protein precu
82	33	53.2	77	2	T20897 hypothetical prote
83	33	53.2	116	1	BVECBA bola protein - Bsc
84	33	53.2	116	2	A90690 probable regulat
85	33	53.2	116	2	B85540 probable murein ge
86	33	53.2	155	2	A28083 glutathione transf
87	33	53.2	162	2	B90402 hypothetical prote
88	33	53.2	181	2	S75415 probable ribosomal
89	33	53.2	196	1	G88P84 basophilic protein
90	33	53.2	217	1	A46630 NADH2 dehydrogenas
91	33	53.2	228	1	OXASC sfah protein precu
92	33	53.2	291	2	S15927 UTP-glucose-1-phos
93	33	53.2	297	2	H70446 F1652 minor fibri
94	33	53.2	299	2	I76900 hypothetical prote
95	33	53.2	302	2	DB1393 probable exporte
96	33	53.2	302	2	T45937 hypothetical prote
97	33	53.2	306	2	AC0602 hypothetical prote
98	33	53.2	306	2	H90740 yb1s protein precu
99	33	53.2	306	2	C64819 hypothetical prote
100	33	53.2	306	2	C85591
101	33	53.2	309	2	AB0757
102	33	53.2			

glutamate-ammonia  
glutamate synthase  
acylaminoacyl-pept  
hypothetical prote  
hypothetical prote  
Iga-specific metal  
hypothetical prote  
fatty-acyl-CoA sym  
hypothetical prote  
unknown protein f  
hypothetical prote  
hypothetical prote  
probable 2-oxoglut  
hypothetical prote  
oxidase like prote  
hypothetical prote  
penicillin-binding  
hypothetical prote  
conserved hypothet  
ATP-dependent RNA  
dipeptidase (impor  
glutamate-ammonia  
hypothetical prote  
hypothetical prote  
H+-exporting ATPas  
hypothetical prote  
outer membrane cha  
hypothetical prote  
protein C43E1.10  
carboxypeptidase C  
oligopeptide ABC t  
fibronectin-bindin  
oligopeptide ABC t  
hypothetical prote  
glucose oxidase (B  
probable PPE prote  
hypothetical prote  
NAD-dependent mal  
isoguinoline 1-oxi  
ubiquitin-specific  
G protein-coupled  
hypothetical prote  
unknown protein f  
glutamate synthase  
probable PPE prote  
hypothetical 367K  
phenazine biosynth  
jacalin beta-1 cha  
hypothetical prote  
bola protein - Bsc  
probable regulator  
probable murein ge  
glutathione transf  
hypothetical prote  
probable ribosomal  
basophilic protein  
NADH2 dehydrogenas  
sfah protein precu  
UTP-glucose-1-phos  
F1652 minor fibri  
hypothetical prote  
probable exporte  
hypothetical prote  
yb1s protein precu  
hypothetical prote  
probable exporte

103	33	53.2	310	2	A99977
104	33	53.2	310	2	B68823
105	33	53.2	310	2	B68823
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108	33	53.2	310	2	B68823
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143	33	53.2	310	2	B68823
144	33	53.2	310	2	B68823
145	33	53.2	310	2	B68823
146	33	53.2	310	2	B68823
147	33	53.2	310	2	B68823
148	33	53.2	310	2	B68823
149	33	53.2	310	2	B68823
150	33	53.2	310	2	B68823
151	33	53.2	310	2	B68823
152	33	53.2	310	2	B68823
153	33	53.2	310	2	B68823
154	33	53.2	310	2	B68823
155	33	53.2	310	2	B68823
156	33	53.2	310	2	B68823
157	33	53.2	310	2	B68823
158	33	53.2	310	2	B68823
159	33	53.2	310	2	B68823
160	33	53.2	310	2	B68823
161	33	53.2	310	2	B68823
162	33	53.2	310	2	B68823
163	33	53.2	310	2	B68823
164	33	53.2	310	2	B68823
165	33	53.2	310	2	B68823
166	33	53.2	310	2	B68823
167	33	53.2	310	2	B68823
168	33	53.2	310	2	B68823
169	33	53.2	310	2	B68823
170	33	53.2	310	2	B68823
171	33	53.2	310	2	B68823
172	33	53.2	310	2	B68823
173	33	53.2	310	2	B68823
174	33	53.2	310	2	B68823
175	33	53.2	310	2	B68823

hypothetical prote  
hypothetical prote  
hypothetical prote  
probable enzyme li  
probable enzyme yb  
Yb18 protein - Bsc  
hypothetical prote  
conserved hypothet  
oligopeptidase ABC t  
D-alanyl-D-alanine  
hypothetical prote  
D-alanyl-D-alanine  
hypothetical prote  
UDP-N-acetylglucos  
arsenical pump mem  
major early-transc  
ME53 orf139 - Bomb  
hypothetical prote  
probable chitinase  
L2 protein - human  
glutamine syntheta  
glutamate-ammonia  
hypothetical prote  
hypothetical prote  
H+-transporting tw  
H+-transporting tw  
H+-exporting ATPas  
nitrogen fixation  
probable exa/hnf  
probable outer mem  
hypothetical prote  
protein T4012.24 l  
hypothetical prote  
hypothetical prote  
phosphotransferase  
phosphotransferase  
PBP-protein phosph  
H91039  
phosphotransferase  
alkaline proteinase  
hypothetical prote  
probable cystathio  
kinesin-like prote  
T44194  
hypothetical prote  
Down-syndrome-crit  
phosphoribosylform  
probable membrane  
riophry complex po  
neurotrophic recep  
hypothetical prote  
sensory transducti  
DNA polymerase III  
soluble starch SYN  
probable helicase  
glycosidase homo  
protein-tyrosine k  
hypothetical prote  
199.6K hypothetical  
lysine-specific cy  
hypothetical prote  
TATA box binding p  
hypothetical prote  
hemagglutinin A -  
hypothetical prote  
AAS surface protei  
oppf homolog, kgmb

176	32	51.6	105	2	A10557
177	32	51.6	105	2	B84974
178	32	51.6	116	2	AB2360
179	32	51.6	145	2	T22693
180	32	51.6	170	2	AF3369
181	32	51.6	186	2	T50361
182	32	51.6	207	2	C83875
183	32	51.6	211	2	AF0175
184	32	51.6	223	2	UC5903
185	32	51.6	231	2	G70439
186	32	51.6	232	2	G70738
187	32	51.6	251	2	B82027
188	32	51.6	252	2	B90194
189	32	51.6	275	2	UC6181
190	32	51.6	278	2	T19813
191	32	51.6	281	2	T38802
192	32	51.6	307	2	B90402
193	32	51.6	319	2	A10307
194	32	51.6	322	2	B64382
195	32	51.6	325	2	C69805
196	32	51.6	327	2	F90180
197	32	51.6	339	2	G75529
198	32	51.6	341	2	T41450
199	32	51.6	354	2	B70663
200	32	51.6	357	2	H83167
201	32	51.6	367	2	H97115
202	32	51.6	370	2	I40085
203	32	51.6	386	2	KMECPW
204	32	51.6	386	2	B85906
205	32	51.6	389	2	F91061
206	32	51.6	389	2	B42708
207	32	51.6	389	2	S20753
208	32	51.6	389	2	S20749
209	32	51.6	391	2	C71302
210	32	51.6	397	2	S42039
211	32	51.6	408	2	G83406
212	32	51.6	418	2	T47239
213	32	51.6	422	2	AF0072
214	32	51.6	433	2	A56953
215	32	51.6	446	2	T01524
216	32	51.6	467	2	AG1059
217	32	51.6	467	2	H88493
218	32	51.6	472	2	B83005
219	32	51.6	475	2	F81208
220	32	51.6	479	2	D86651
221	32	51.6	479	2	UQ0781
222	32	51.6	481	2	F82432
223	32	51.6	481	2	T46606
224	32	51.6	497	2	T19077
225	32	51.6	528	2	ALBSK
226	32	51.6	534	2	S71300
227	32	51.6	534	2	S71300
228	32	51.6	538	2	G60885
229	32	51.6	540	2	B40901
230	32	51.6	547	2	C84593
231	32	51.6	554	2	B82934
232	32	51.6	558	2	E70756
233	32	51.6	560	2	A86214
234	32	51.6	574	2	G83794
235	32	51.6	575	2	AC0364
236	32	51.6	599	2	S15004
237	32	51.6	610	2	G86407
238	32	51.6	613	2	T19677
239	32	51.6	619	2	B82141
240	32	51.6	633	2	A26030
241	32	51.6	637	2	YCRP
242	32	51.6	638	2	S22490
243	32	51.6	638	2	S22491
244	32	51.6	652	2	S29838
245	32	51.6	655	2	S17691
246	32	51.6	655	2	AS4872
247	32	51.6	659	2	S60056
248	32	51.6	659	2	S60056

Bola protein (limp  
protein-export mem  
hypothetical prote  
hypothetical prote  
xanthine phosphori  
hypothetical prote  
hypothetical prote  
conserved hypothet  
coat protein - Cym  
DNA repair protein  
probable MAFB alte  
probable MAFB alte  
phosphate ABC tran  
RNA polymerase II  
hypothetical prote  
hypothetical prote  
flagellin, probabl  
formylmethanofuran  
iron(III) dicitrat  
sun (fmu) protein  
peptide ABC transp  
hypothetical prote  
probable PPE prote  
b10b/LiPA-like pro  
probable transfe  
gcs protein - Bac  
chorismate mutase  
probable hydrocarb  
chorismate mutase-  
serine-type D-Ala-  
surface antigen -  
probable exonuclea  
hypothetical prote  
conserved hypothet  
oxalate/formate an  
probable symporter  
transcription fact  
zinc finger protei  
probable membrane  
protein F57B9.10 l  
glutamate syntheta  
glutamate-ammonia  
polysaccharide bio  
sucrose uptake pro  
PTS system, sucros  
cell cycle control  
hypothetical prote  
alpha-amylase (Bc  
hypothetical prote  
regulatory protein  
hypothetical prote  
equine arteritis v  
probable sugar tra  
hypothetical prote  
hypothetical glyci  
hypothetical prote  
phosphoenolpyruv  
acetylactate synth  
hypothetical prote  
hypothetical prote  
peptidyl-prolyl ci  
serine/chreonine-s  
acetylactate synth  
acetylactate synth  
acetylactate synth  
acetylactate synth  
acyl-CoA dehydroge  
acetylactate synth

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:05 ; Search time 76.2857 Seconds  
(without alignments)  
129.479 Million cell updates/sec

Title: US-10-067-484-1  
Perfect score: 62  
Sequence: 1 XXSGISNTVYANPK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : UniProt 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	69.4	666	2	05VGY1_PLAFA
2	43	69.4	666	2	05VGY1_plasmodium
3	43	69.4	666	2	081A26_PLAFA
4	42	67.7	242	2	0815W4_PLAFA
5	42	67.7	242	2	05SPD1_CRYNE
6	42	67.7	242	2	05KE25_CRYNE
7	42	67.7	540	2	04MP87_BACCE
8	42	67.7	540	2	06HBP3_BACCH
9	42	67.7	540	2	081CC5_BACCR
10	42	67.7	540	2	081FP9_BACAN
11	42	67.7	899	2	063AA2_BACCE
12	42	67.7	899	2	04N9L5_THBPA
13	42	67.7	1242	2	04X2J9_PLACH
14	41	66.1	75	2	05BQZ4_SCHUA
15	41	66.1	106	2	04VC39_HUMAN
16	41	66.1	382	2	09KCB8_BACAN
17	41	66.1	1972	2	06MS19_MYCMS
18	40	64.5	355	2	07UP11_RHOBA
19	40	64.5	769	2	08MSK2_TRYBB
20	40	64.5	769	2	04P7V3_USUMA
21	40	64.5	1098	2	05OPJ3_ENTHI
22	39	62.9	106	2	09BW72_HUMAN
23	39	62.9	106	2	09CQJ1_MOUSE
24	39	62.9	229	2	04YV99_PLACH
25	39	62.9	229	2	04YV99_PLACH
26	39	62.9	258	2	04FMB9_GRICK
27	39	62.9	258	2	08RGL2_FUSYN
28	39	62.9	276	2	07RXX7_PLAFA
29	39	62.9	278	2	081DP1_PLAFA
30	39	62.9	342	2	07RK05_PLAFA
31	39	62.9	584	2	08RGS8_FUSNN

32	39	62.9	639	2	094B28_ARATH	094b28 arabidopsis
33	39	62.9	655	2	0869S4_DICDI	0869s4 dictyostel
34	39	62.9	673	2	091E59_ARATH	091e59 arabidopsis
35	39	62.9	688	2	0554Z5_DICDI	0554z5 dictyostel
36	39	62.9	796	2	05NRA2_ZYMO	05nra2 zymomonas
37	39	62.9	905	2	04UG55_THBAN	04ug55 theileria
38	39	62.9	1024	1	Y075_MYCB	Y47321 mycoplasma
39	39	62.9	1476	2	08TFN3_NEUCR	08tfn3 neurospora
40	39	62.9	1520	2	07S8U6_NEUCR	07s8u6 neurospora
41	38	61.3	67	2	07P3N2_FUSNV	07p3n2 fusobacteri
42	38	61.3	99	2	05VOC7_HALMA	05voc7 haloarcula
43	38	61.3	125	2	04WVX3_BACE	04wvx3 bacillus ce
44	38	61.3	204	2	071AE7_9NOCL	071ae7 manesstra co
45	38	61.3	204	2	08QLG9_NPYMC	08qlg9 manesstra co
46	38	61.3	258	2	05GRV9_WOLTR	05grv9 wolbachia s
47	38	61.3	314	2	0658X8_HUMAN	0658x8 homo sapien
48	38	61.3	315	2	06ERF6_XENTA	06erf6 xenopus lae
49	38	61.3	315	2	06CAL3_YARLI	06cal3 yarrowia ii
50	38	61.3	323	2	09H635_HUMAN	09h635 homo sapien
51	38	61.3	333	2	09P5R5_VIBCH	09p5r5 vibrio chol
52	38	61.3	336	2	09KTI0_VIBCH	09kti0 mus muscucu
53	38	61.3	356	1	ASCC1_MOUSE	09ad821 mus muscucu
54	38	61.3	356	2	05XII1_PAT	05xii1 rattus norv
55	38	61.3	380	2	05WGG2_BACSK	05wgg2 bacillus cl
56	38	61.3	400	2	06CFI7_YARLI	06cfi7 yarrowia ii
57	38	61.3	432	2	0874D8_ORPSP	0874d8 orpinomyces
58	38	61.3	432	2	0874E0_ORPSP	0874e0 orpinomyces
59	38	61.3	459	2	055FP6_DICDI	055fp6 dictyostel
60	38	61.3	512	2	05RCY4_PONPY	05rcy4 pongo pygma
61	38	61.3	522	2	08R585_MOUSE	08r585 mus muscucu
62	38	61.3	635	2	04R6K0_MACFA	04r6k0 macaca faec
63	38	61.3	690	2	08BP56_MOUSE	08bp56 m mus muscu
64	38	61.3	910	2	0591W8_CANAL	0591w8 candida alb
65	38	61.3	1001	2	05A3N0_CANAL	05a3n0 candida alb
66	38	61.3	1012	2	05A3U5_CANAL	05a3u5 aspergillus
67	38	61.3	1031	2	05G612_EMENI	05g612 dictyostel
68	38	61.3	1137	2	055CG8_DICDI	055cg8 dictyostel
69	38	61.3	1542	2	07SFA8_NEUCR	07sfa8 neurospora
70	37	59.7	93	1	Y100_ARCFU	030136 archaeoglob
71	37	59.7	127	2	05ICJ4_BACFN	05icj4 bacteroides
72	37	59.7	127	2	06ATP3_BACFR	06atp3 bacteroides
73	37	59.7	204	2	08UM88_9NOCL	08um88 manesstra co
74	37	59.7	223	2	06UTY3_YVIRU	06uty3 cyndidium m
75	37	59.7	223	2	06UTY4_YVIRU	06uty4 arabidopsis
76	37	59.7	234	2	05XVD4_ARATH	05xvd4 arabidopsis
77	37	59.7	257	2	073IK7_WOLPM	073ik7 wolbachia p
78	37	59.7	268	2	041172_AZOVI	041172 azotobacter
79	37	59.7	297	2	07RGD5_PLAFA	07rgd5 plasmodium
80	37	59.7	319	2	06BQZ9_DEBHA	06bz25 debaryomyce
81	37	59.7	321	2	07RSQ0_PLAFA	07rsq0 plasmodium
82	37	59.7	321	2	05BPS8_ARATH	05bps8 arabidopsis
83	37	59.7	323	2	05YVD5_ARATH	05yvd5 arabidopsis
84	37	59.7	336	2	05FP05_GUOX	05fp05 gluconobact
85	37	59.7	339	2	09XIN9_ARATH	09xin9 arabidopsis
86	37	59.7	376	2	09P808_9FUNG	09p8q8 piromyces t
87	37	59.7	389	2	05F9F3_NEIG1	05f9f3 neisseria g
88	37	59.7	389	2	09JUX6_NEIMA	09jux6 neisseria m
89	37	59.7	389	2	09JWZ2_NEIMA	09jwz2 neisseria m
90	37	59.7	409	2	07BR32_STRCL	07br32 streptomyce
91	37	59.7	412	2	06EH22_NEORF	06eh22 neocallimas
92	37	59.7	414	2	09VBS3_DROME	09vbs3 dirosophila
93	37	59.7	428	2	012646_NEOPA	012646 neocallimas
94	37	59.7	429	2	06EY63_9FUNG	06ey63 neocallimas
95	37	59.7	474	2	08KCZ2_CHLRE	08kc22 chlorobact
96	37	59.7	484	2	07VE91_HELHP	07ve91 helicobacte
97	37	59.7	498	2	057ZFS_9TRIP	057zfs trypanosoma
98	37	59.7	510	2	06E1Y8_NEOFR	06e1y8 neocallimas
99	37	59.7	550	2	04KKU3_HUMAN	04kku3 homo sapien
100	37	59.7	562	1	KPYG_TOBAC	040546 nicotiana t
101	37	59.7	574	2	053W57_TORAC	053w57 nicotiana t
102	37	59.7	586	2	06FPZ1_CANGA	06fpz1 candida gla
103	37	59.7	586	2	04WDB8_ASFPU	04wdb8 aspergillus
104	37	59.7	589	2	07WBQ2_BORPA	07wbq2 bordetella

105	37	59.7	589	2	Q7MM6 BORBR	Q7mb6 bordelella	178	36	58.1	598	2	Q4XMR4 PLACH	Q4xmr4 plasmodium
106	37	59.7	589	2	Q7MM6 BORBR	Qmb6 caulifex ariet	179	36	58.1	598	2	Q7XMR0 NEUCR	Q7xmr0 neurospora
107	37	59.7	653	2	Q67097 ACUAR	Q67097 acuar	180	36	58.1	607	2	Q17795 CAEBL	Q17795 caenorhabd
108	37	59.7	696	2	Q54201 STRCL	Q54201 streptomyc	181	36	58.1	607	2	Q7XMR0 NEUCR	Q7xmr0 neurospora
109	37	59.7	728	2	Q7R178 PLAYO	Q7r178 plasmodium	182	36	58.1	644	2	Q81227 PLAF7	Q81227 plasmodium
110	37	59.7	795	2	Q4KJ53 PSBFS	Q4kj53 pseudomonas	183	36	58.1	695	2	Q652K2 ORSYA	Q652K2 oryza sativ
111	37	59.7	828	2	Q4ZWN7 PSBSE	Q4zwn7 pseudomonas	184	36	58.1	702	2	Q5UPL2 MINIV	Q5upl2 mimivir
112	37	59.7	831	2	Q4ZWN7 PSBSE	Q4zwn7 pseudomonas	185	36	58.1	717	2	Q61F0 DROME	Q61f0 drosophila
113	37	59.7	831	2	Q4ZWN7 PSBSE	Q4zwn7 pseudomonas	186	36	58.1	756	2	Q624H3 CAEBR	Q624h3 caenorhabd
114	37	59.7	955	2	Q4VW4 ORYSA	Q4vw4 oryza sativ	187	36	58.1	766	2	Q8MOE6 CAEBL	Q8moE6 caenorhabd
115	37	59.7	972	2	Q4VW4 ORYSA	Q4vw4 oryza sativ	188	36	58.1	786	2	Q7RUI3 PLAYO	Q7riu3 plasmodium
116	37	59.7	972	2	Q4VW4 ORYSA	Q4vw4 oryza sativ	189	36	58.1	816	2	Q4FW40 LEIMA	Q4fw40 leishmania
117	37	59.7	1012	2	Q6ZV8 HUMAN	Q6zV8 homo sapien	190	36	58.1	879	2	Q5AT77 EMENI	Q5at77 emenilla
118	37	59.7	1012	2	Q6ZV8 HUMAN	Q6zV8 homo sapien	191	36	58.1	883	2	Q5AT77 EMENI	Q5at77 emenilla
119	37	59.7	1197	2	Q6ZV8 HUMAN	Q6zV8 homo sapien	192	36	58.1	933	2	Q7SSB3 NEUCR	Q7ssb3 neurospora
120	37	59.7	1220	2	Q6XK05 NEUCR	Q6xk05 neurospora	193	36	58.1	1002	2	Q4HMS5 CIOIN	Q4hms5 clostridia
121	37	59.7	1220	2	Q6XK05 NEUCR	Q6xk05 neurospora	194	36	58.1	1128	2	Q6KNR9 DROME	Q6knr9 drosophila
122	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	195	36	58.1	1135	2	Q6KNR9 DROME	Q6knr9 drosophila
123	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	196	36	58.1	1138	2	Q6KNR9 DROME	Q6knr9 drosophila
124	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	197	36	58.1	1180	2	Q6KNR9 DROME	Q6knr9 drosophila
125	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	198	36	58.1	1180	2	Q6KNR9 DROME	Q6knr9 drosophila
126	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	199	36	58.1	1227	2	Q6KNR9 DROME	Q6knr9 drosophila
127	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	200	36	58.1	1227	2	Q6KNR9 DROME	Q6knr9 drosophila
128	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	201	36	58.1	1227	2	Q6KNR9 DROME	Q6knr9 drosophila
129	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	202	36	58.1	1227	2	Q6KNR9 DROME	Q6knr9 drosophila
130	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	203	36	58.1	1227	2	Q6KNR9 DROME	Q6knr9 drosophila
131	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	204	36	58.1	1227	2	Q6KNR9 DROME	Q6knr9 drosophila
132	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	205	36	58.1	1227	2	Q6KNR9 DROME	Q6knr9 drosophila
133	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	206	36	58.1	1227	2	Q6KNR9 DROME	Q6knr9 drosophila
134	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk05 neurospora	207	36	58.1	1227	2	Q6KNR9 DROME	Q6knr9 drosophila
135	37	59.7	1222	2	Q6XK05 NEUCR	Q6xk							

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:21 ; Search time 27.1429 Seconds  
(without alignments)  
42.643 Million cell updates/sec

Title: US-10-067-484-1

Perfect score: 62

Sequence: 1 XXSGISNYYANPK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5.COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/6.COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/H.COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/PCTUS.COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/RT.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
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3	39	62.9	474	2	US-09-758-759-39
4	39	62.9	637	2	US-09-489-039A-9243
5	39	62.9	858	1	US-07-712-284-2
6	39	62.9	858	4	PCT-US92-04227-2
7	39	62.9	1024	2	US-09-091-117-5
8	38	61.3	66	2	US-09-248-796A-21394
9	38	61.3	432	2	US-09-118-319-2
10	38	61.3	432	2	US-10-070-634-2
11	37	59.7	336	2	US-09-286-591-23
12	37	59.7	336	2	US-09-687-147-23
13	37	59.7	332	2	US-09-428-034-4
14	37	59.7	376	2	US-09-428-034-2
15	37	59.7	428	2	US-09-118-319-5
16	37	59.7	515	2	US-09-107-532A-5317
17	37	59.7	700	2	US-09-620-412C-345
18	37	59.7	700	2	US-09-598-419-345
19	37	59.7	712	1	US-08-468-576B-17
20	37	59.7	712	1	US-08-468-576B-17
21	37	59.7	712	2	US-08-468-576B-17
22	37	59.7	841	2	US-09-252-991A-33134
23	37	59.7	1397	2	US-10-157-220-174
24	37	59.7	1752	2	US-09-556-877-180
25	37	59.7	1752	2	US-09-620-412C-180
26	37	59.7	1752	2	US-09-598-419-180
27	36	58.1	297	2	US-09-107-532A-5306

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30	36	58.1	1180	4	PCT-US94-07902-28	Sequence 28, Appl
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34	35	56.5	256	2	US-09-270-767-47710	Sequence 47710, A
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53	34	54.8	352	2	US-09-543-681A-4723	Sequence 4723, Ap
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106	33	53.2	763	2	US-08-789-275-4	Sequence 4, Appl1	179	32	51.6	469	2	US-09-602-787A-134	Sequence 134, App
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117	33	53.2	1197	2	US-09-606-304-12	Sequence 35, Appl1	191	32	51.6	599	1	US-08-455-355-1	Sequence 1, Appl1
118	33	53.2	1230	2	US-08-968-542C-35	Sequence 35, Appl1	192	32	51.6	599	1	US-08-455-355-3	Sequence 2, Appl1
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120	33	53.2	1230	2	US-07-813-593-4	Sequence 6, Appl1	194	32	51.6	599	1	US-09-367-512-1	Sequence 1, Appl1
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145	33	53.2	1230	2	US-09-919-408A-6	Sequence 6, Appl1	219	32	51.6	633	2	US-10-407-339-3	Sequence 3, Appl1
146	33	53.2	1230	2	US-09-919-408A-6	Sequence 6, Appl1	220	32	51.6	633	2	US-10-407-339-3	Sequence 3, Appl1
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173	33	53.2	1230	2	US-09-919-408A-6	Sequence 6, Appl1	247	32	51.6	633	2	US-10-407-339-3	Sequence 3, Appl1



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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:50:47 ; Search time 67.4286 Seconds  
(without alignments)  
86.753 Million cell updates/sec

Title: US-10-067-484-1

Perfect score: 62

Sequence: 1 XXSGISNTVYANPK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:\*

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- 4: /cgn2\_6/pcodata/1/pubppa/US10A\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	62	100.0	14	US-10-067-484-1
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6	39	62.9	278	US-10-732-923-18495
7	39	62.9	401	US-09-769-734-7
8	39	62.9	474	US-09-758-759-39
9	39	62.9	474	US-11-021-825-39
10	39	62.9	489	US-10-107-431-237
11	39	62.9	490	US-10-282-122A-59142
12	39	62.9	493	US-10-107-431-239
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15	38	61.3	339	US-10-282-122A-77223
16	38	61.3	552	US-10-369-493-20174
17	38	61.3	552	US-10-322-281-732
18	38	61.3	602	US-10-450-763-33261
19	38	61.3	697	US-10-322-281-729
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24	37	59.7	700	US-10-872-155-345
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26	37	59.7	831	US-10-282-122A-69302
27	37	59.7	955	US-10-437-963-149675

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36	37	59.7	1751	US-10-872-155-594	Sequence 594, App
37	37	59.7	1751	US-10-498-327-115	Sequence 115, App
38	37	59.7	1751	US-10-503-135-119	Sequence 119, App
39	37	59.7	1752	US-09-841-132-180	Sequence 180, App
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:04 ; Search time 12.2857 Seconds

(without alignments)  
48.418 Million cell updates/sec

Title: US-10-067-484-1

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42469236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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38	34	54.8	314	7	US-11-188-298-16630	Sequence 16630, A
39	34	54.8	390	7	US-10-510-386-158	Sequence 158, App
40	34	54.8	390	7	US-11-079-463-9948	Sequence 9948, App
41	34	54.8	476	7	US-11-188-298-7595	Sequence 7595, App
42	34	54.8	495	7	US-11-052-554A-69	Sequence 69, App1
43	34	54.8	496	7	US-11-188-298-5891	Sequence 5891, App
44	34	54.8	532	7	US-11-188-298-16230	Sequence 16230, A
45	34	54.8	685	7	US-11-188-298-16230	Sequence 9916, App
46	34	54.8	3300	7	US-11-052-554A-133	Sequence 133, App
47	33	53.2	158	7	US-11-188-298-1739	Sequence 1739, App
48	33	53.2	297	7	US-11-188-298-15412	Sequence 15412, A
49	33	53.2	379	6	US-10-513-759-12	Sequence 12, App1
50	33	53.2	413	6	US-10-530-773-215	Sequence 215, App
51	33	53.2	419	7	US-11-188-298-2553	Sequence 2553, App
52	33	53.2	419	7	US-11-188-298-3683	Sequence 3683, App
53	33	53.2	419	7	US-11-188-298-9538	Sequence 9538, App
54	33	53.2	419	7	US-11-188-298-15412	Sequence 15412, A
55	33	53.2	419	7	US-11-188-298-17599	Sequence 17599, A
56	33	53.2	447	7	US-11-188-298-17635	Sequence 12635, A
57	33	53.2	451	7	US-11-188-298-784	Sequence 784, App
58	33	53.2	451	7	US-11-188-298-5686	Sequence 5686, App
59	33	53.2	451	7	US-11-188-298-11603	Sequence 11603, A
60	33	53.2	451	7	US-11-188-298-13655	Sequence 13655, A
61	33	53.2	451	7	US-11-188-298-20758	Sequence 20758, A
62	33	53.2	451	7	US-11-188-298-21698	Sequence 21698, A
63	33	53.2	462	7	US-11-079-463-10049	Sequence 10049, A
64	33	53.2	465	7	US-11-188-298-3566	Sequence 3566, App
65	33	53.2	468	7	US-11-188-298-7563	Sequence 7563, App
66	33	53.2	468	7	US-11-188-298-13522	Sequence 13522, A
67	33	53.2	468	7	US-11-188-298-8439	Sequence 8439, App
68	33	53.2	468	7	US-11-188-298-14314	Sequence 14314, A
69	33	53.2	468	7	US-11-188-298-14314	Sequence 14314, A
70	33	53.2	468	7	US-11-188-298-16463	Sequence 16463, A
71	33	53.2	468	7	US-11-188-298-21559	Sequence 21559, A
72	33	53.2	469	7	US-11-188-298-19006	Sequence 19006, A
73	33	53.2	472	7	US-11-188-298-3521	Sequence 3521, App
74	33	53.2	472	7	US-11-188-298-17810	Sequence 17810, A
75	33	53.2	472	7	US-11-188-298-19933	Sequence 19933, A
76	33	53.2	473	7	US-11-188-298-1923	Sequence 1923, App
77	33	53.2	473	7	US-11-188-298-5810	Sequence 5810, App
78	33	53.2	473	7	US-11-188-298-7082	Sequence 7082, App
79	33	53.2	473	7	US-11-188-298-19070	Sequence 19070, A
80	33	53.2	474	7	US-11-188-298-14501	Sequence 14501, A
81	33	53.2	506	6	US-11-188-298-3406	Sequence 3406, App
82	33	53.2	524	6	US-10-467-657-8258	Sequence 8258, App
83	33	53.2	556	7	US-11-096-568A-27991	Sequence 27991, A
84	33	53.2	594	7	US-11-096-568A-27990	Sequence 27990, A
85	33	53.2	654	7	US-11-096-568A-27989	Sequence 27989, A
86	33	53.2	766	6	US-10-821-334-1691	Sequence 1691, App
87	33	53.2	960	7	US-11-169-041-1177	Sequence 1177, App
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89	33	53.2	1343	6	US-10-541-814-15	Sequence 15, App1
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91	33	53.2	1678	7	US-11-124-367A-340	Sequence 341, App
92	33	53.2	1678	7	US-11-124-367A-341	Sequence 173, App
93	33	53.2	2105	7	US-11-052-554A-133	Sequence 7036, App
94	32	52.4	386	7	US-11-079-463-7036	Sequence 53, App1
95	32	51.6	42	6	US-10-957-8879-53	Sequence 14383, A
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97	32	51.6	202	7	US-11-188-298-10344	Sequence 900, App
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101	32	51.6	348	6	US-10-821-234-1514	Sequence 1514, Ap	174	32	51.6	655	7	US-11-079-132-13	Sequence 13, Appl
102	32	51.6	348	6	US-10-857-780-24	Sequence 24, Appl	175	32	51.6	655	7	US-11-079-132-15	Sequence 15, Appl
103	32	51.6	348	7	US-11-108-088-58	Sequence 58, Appl	176	32	51.6	655	7	US-11-188-298-21509	Sequence 21509, A
104	32	51.6	354	7	US-11-052-086-65	Sequence 65, Appl	177	32	51.6	656	7	US-11-076-733-25	Sequence 25, Appl
105	32	51.6	354	7	US-11-087-099-8289	Sequence 156, Appl	178	32	51.6	656	7	US-11-198-728-22	Sequence 22, Appl
106	32	51.6	361	7	US-11-149-348-4393	Sequence 439, Appl	179	32	51.6	656	7	US-11-149-420-24	Sequence 24, Appl
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121	32	51.6	541	7	US-11-188-298-1088	Sequence 9885, Ap	194	32	51.6	667	7	US-11-188-298-15770	Sequence 15770, A
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123	32	51.6	555	7	US-11-188-298-10168	Sequence 10168, A	196	32	51.6	668	7	US-11-188-298-21795	Sequence 21795, A
124	32	51.6	567	7	US-11-188-298-14477	Sequence 18477, A	197	32	51.6	669	7	US-11-188-298-4171	Sequence 4171, Ap
125	32	51.6	577	7	US-11-188-298-15593	Sequence 9567, Ap	198	32	51.6	669	7	US-11-188-298-13639	Sequence 13639, A
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127	32	51.6	583	7	US-11-188-298-4277	Sequence 795, Ap	200	32	51.6	670	7	US-11-188-298-17459	Sequence 17459, A
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130	32	51.6	583	7	US-11-188-298-3313	Sequence 3313, Ap	203	32	51.6	670	7	US-11-188-298-21602	Sequence 21602, A
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132	32	51.6	583	7	US-11-188-298-3313	Sequence 3313, Ap	205	32	51.6	670	7	US-11-188-298-21602	Sequence 21602, A
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154	32	51.6	583	7	US-11-188-298-3313	Sequence 3313, Ap	227	32	51.6	670	7	US-11-188-298-21602	Sequence 21602, A
155	32	51.6	583	7	US-11-188-298-3313	Sequence 3313, Ap	228	32	51.6	670	7	US-11-188-298-21602	Sequence 21602, A
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163	32	51.6	583	7	US-11-188-298-3313	Sequence 3313, Ap	236	32	51.6	670	7	US-11-188-298-21602	Sequence 21602, A
164	32	51.6	583	7	US-11-188-298-3313	Sequence 3313, Ap	237	32	51.6	670	7	US-11-188-298-21602	Sequence 21602, A
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168	32	51.6	583	7	US-11-188-298-3313	Sequence 3313, Ap	241	32	51.6	670	7	US-11-188-298-21602	Sequence 21602, A
169	32	51.6	583	7	US-11-188-298-3313	Sequence 3313, Ap	242	32	51.6	670	7	US-11-188-298-21602	Sequence 21602, A
170	32	51.6	583	7	US-11-188-298-3313	Sequence 3313, Ap	243	32	51.6	670	7	US-11-188-298-21602	Sequence 21602, A
171	32	51.6	583	7	US-11-188-298-3313	Sequence 3313, Ap	244	32	51.6	670	7	US-11-188-298-21602	Sequence 21602, A

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:40:47 ; Search time 90.7347 Seconds  
(without alignments) 43.582 Million cell updates/sec

Title: US-10-067-484-2  
Perfect score: 42  
Sequence: 1 PRSFXMXATK 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

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2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	33	78.6	271	3	AAU10010
5	33	78.6	345	4	ABH60198
6	32	76.2	158	8	ADK78345
7	32	76.2	232	7	ABO60780
8	32	76.2	360	4	AAW41900
9	32	76.2	663	4	ABH52462
10	32	76.2	713	7	ADCO1362
11	32	76.2	713	9	AEH91364
12	32	76.2	808	7	ADJ68916
13	32	76.2	2194	4	AAW40114
14	32	76.2	2829	8	ADL72180
15	31	73.8	110	4	AAB62783
16	31	73.8	126	4	ABG02725
17	31	73.8	457	4	ABH69700
18	31	73.8	1361	6	ABU20358
19	31	73.8	6815	4	ABH66811
20	30	71.4	85	1	AAU70412
21	30	71.4	100	2	AAU35084
22	30	71.4	110	6	ABP60080
23	30	71.4	154	7	ABO65493
24	30	71.4	187	4	ABG04966

25	30	71.4	214	7	ADH86644	Adh86644 Enterococ
26	30	71.4	287	7	ABO74345	ABO74345 Pseudomon
27	30	71.4	319	4	AAU63426	AAU63426 Propionib
28	30	71.4	319	6	ABH65512	ABH65512 Propionib
29	30	71.4	319	6	ABH59945	ABH59945 Propionib
30	30	71.4	371	8	ADN24100	ADN24100 Bacterial
31	30	71.4	407	6	ABU37853	ABU37853 Protein e
32	30	71.4	418	5	ABH06969	ABH06969 Canine AS
33	30	71.4	426	6	ABP77795	ABP77795 N. gonorr
34	30	71.4	426	6	ABU37534	ABU37534 Protein e
35	30	71.4	441	6	ADH35082	ADH35082 Actinobac
36	30	71.4	851	8	ADQ66949	ADQ66949 Novel hum
37	30	71.4	870	2	AAU31348	AAU31348 Jaagsiek
38	30	71.4	987	8	ADL05331	ADL05331 M. catarr
39	30	71.4	1362	6	ABU17069	ABU17069 Protein e
40	30	71.4	1363	6	ABU35175	ABU35175 Protein e
41	30	71.4	1380	6	ADH36845	ADH36845 Actinobac
42	30	71.4	2626	3	ABH07569	ABH07569 Protein e
43	29	69.0	65	4	AAU45762	AAU45762 Propionib
44	29	69.0	65	6	ABM42281	ABM42281 Light cha
45	29	69.0	106	2	AAW71241	AAW71241 Light cha
46	29	69.0	107	9	AEA48149	AEA48149 Mouse ant
47	29	69.0	107	9	AEA48156	AEA48156 Mouse ant
48	29	69.0	107	9	AEA48154	AEA48154 Mouse ant
49	29	69.0	107	9	AEA48155	AEA48155 Mouse ant
50	29	69.0	107	9	AEH13698	AEH13698 Human ant
51	29	69.0	107	9	AEH13703	AEH13703 Human ant
52	29	69.0	107	9	AEH13704	AEH13704 Human ant
53	29	69.0	107	9	AEH13702	AEH13702 Human ant
54	29	69.0	107	9	AEH13700	AEH13700 Human ant
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57	29	69.0	127	2	AAW08941	AAW08941 Kappa lig
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59	29	69.0	178	6	ABH53685	ABH53685 Protein e
60	29	69.0	178	7	ADK64062	ADK64062 Disease t
61	29	69.0	202	5	ABH55266	ABH55266 Lactococc
62	29	69.0	214	9	AEA48169	AEA48169 Mouse ant
63	29	69.0	214	9	AEA48166	AEA48166 Mouse ant
64	29	69.0	233	6	ABU44004	ABU44004 Protein e
65	29	69.0	236	8	ADU14301	ADU14301 EGFR ligh
66	29	69.0	236	8	ADP44635	ADP44635 Murine an
67	29	69.0	236	8	AEA60461	AEA60461 Mouse ant
68	29	69.0	239	2	AAU34511	AAU34511 FV(TU25)
69	29	69.0	240	2	AAW05133	AAW05133 Single ch
70	29	69.0	240	2	AAW71243	AAW71243 scFv comp
71	29	69.0	292	6	ADA34980	ADA34980 Actinobac
72	29	69.0	296	6	ADK88689	ADK88689 Plant ful
73	29	69.0	340	5	ABP40337	ABP40337 Staphyloc
74	29	69.0	340	8	ADU04889	ADU04889 Staphyloc
75	29	69.0	413	6	ABU22839	ABU22839 Protein e
76	29	69.0	417	8	ADL45281	ADL45281 Rice isop
77	29	69.0	487	5	AAU76889	AAU76889 Pneumococ
78	29	69.0	494	6	ABU47959	ABU47959 Protein e
79	29	69.0	494	6	ABU47959	ABU47959 Protein e
80	29	69.0	498	7	ADU13794	ADU13794 Plasmid p
81	29	69.0	500	7	ADU13792	ADU13792 Plasmid p
82	29	69.0	651	2	AAW05135	AAW05135 scFv(225)
83	29	69.0	722	2	ABU27630	ABU27630 Protein e
84	29	69.0	754	8	ADN25644	ADN25644 Bacterial
85	29	69.0	784	8	ADU30331	ADU30331 Bacterial
86	29	69.0	785	9	ABH90808	ABH90808 M. xanthu
87	29	69.0	892	2	AAW05140	AAW05140 scFv2(225
88	29	69.0	892	2	AAW05139	AAW05139 scFv2(FRP
89	29	69.0	913	8	ADN24602	ADN24602 Bacterial
90	29	69.0	924	8	ADN21843	ADN21843 Bacterial
91	29	69.0	935	7	ADH88608	ADH88608 Enterococ
92	29	69.0	946	8	ADN25957	ADN25957 Bacterial
93	29	69.0	1001	6	ABU21679	ABU21679 Protein e
94	29	69.0	1020	2	AAW05141	AAW05141 scFv2(FRP
95	29	69.0	1042	6	ABU22137	ABU22137 Protein e
96	29	69.0	1060	4	ABH64804	ABH64804 Drosophila
97	29	69.0	1172	4	ABH66466	ABH66466 Drosophila

98	29	69.0	1514	2	AAW7390	AAW7390 Mouse add
99	29	69.0	1514	2	AAW7392	AAW7392 Mouse add
100	28	66.7	1514	2	ABG3092	ABG3092 DR2+0101
101	28	66.7	1514	2	AAW2054	AAW2054 Human nor
102	28	66.7	1514	2	AAW8521	AAW8521 SSL deri
103	28	66.7	1514	2	AAW8513	AAW8513 Consensus
104	28	66.7	1514	2	AAW8506	AAW8506 Target an
105	28	66.7	1514	2	AAW8512	AAW8512 Consensus
106	28	66.7	1514	2	AAW8520	AAW8520 SSL deri
107	28	66.7	1514	2	AAW8507	AAW8507 Target an
108	28	66.7	1514	2	AAW8511	AAW8511 Consensus
109	28	66.7	1514	2	AAW8504	AAW8504 Target an
110	28	66.7	1514	2	AAW8510	AAW8510 Consensus
111	28	66.7	1514	2	AAW8505	AAW8505 Target an
112	28	66.7	1514	2	AAW8507	AAW8507 peptide s
113	28	66.7	1514	2	AAW8531	AAW8531 Modified
114	28	66.7	1514	2	AAW91221	AAW91221 Modified
115	28	66.7	1514	2	AAW20833	AAW20833 M-CSF spe
116	28	66.7	1514	2	AAW41875	AAW41875 Arabidops
117	28	66.7	1514	2	ADJ89953	ADJ89953 Foot-and-
118	28	66.7	1514	2	ADJ56912	ADJ56912 Foot-and-
119	28	66.7	1514	2	AAW6608	AAW6608 Peptide s
120	28	66.7	1514	2	AAW68532	AAW68532 Synthetic
121	28	66.7	1514	2	AAW91222	AAW91222 inv epitlo
122	28	66.7	1514	2	AAW7552	AAW7552 Human sec
123	28	66.7	1514	2	AAW7552	AAW7552 Breast sp
124	28	66.7	1514	2	ADJ18366	ADJ18366 Plant ful
125	28	66.7	1514	2	ADJ39862	ADJ39862 Plant ful
126	28	66.7	1514	2	AAW93862	AAW93862 Human gen
127	28	66.7	1514	2	AAW01772	AAW01772 Human gen
128	28	66.7	1514	2	AAW01801	AAW01801 Human gen
129	28	66.7	1514	2	AAW64196	AAW64196 Human gtb
130	28	66.7	1514	2	AAW64197	AAW64197 Human gtb
131	28	66.7	1514	2	ADJ77461	ADJ77461 Albumin f
132	28	66.7	1514	2	AAW87462	AAW87462 S1 epider
133	28	66.7	1514	2	AAW82728	AAW82728 Plant ful
134	28	66.7	1514	2	AAW12493	AAW12493 Plant ful
135	28	66.7	1514	2	AAW40019	AAW40019 Mouse ant
136	28	66.7	1514	2	AAW50190	AAW50190 Anti-LDR
137	28	66.7	1514	2	AAW50190	AAW50190 Light cha
138	28	66.7	1514	2	AAW08948	AAW08948 kappa 119
139	28	66.7	1514	2	AAW08948	AAW08948 kappa 119
140	28	66.7	1514	2	AAW70604	AAW70604 Light cha
141	28	66.7	1514	2	AAW70604	AAW70604 V kappa re
142	28	66.7	1514	2	ADJ80370	ADJ80370 Antibody
143	28	66.7	1514	2	ADJ80370	ADJ80370 FR homolo
144	28	66.7	1514	2	ADJ66055	ADJ66055 C. glutam
145	28	66.7	1514	2	ADJ7028	ADJ7028 TAIL-27d2
146	28	66.7	1514	2	ADJ43467	ADJ43467 Light cha
147	28	66.7	1514	2	ADJ43467	ADJ43467 Mutine an
148	28	66.7	1514	2	ADJ43469	ADJ43469 Light cha
149	28	66.7	1514	2	ADJ43465	ADJ43465 Light cha
150	28	66.7	1514	2	ADJ43461	ADJ43461 Light cha
151	28	66.7	1514	2	ADJ43457	ADJ43457 Light cha
152	28	66.7	1514	2	ADJ43463	ADJ43463 Heavy cha
153	28	66.7	1514	2	ADJ1610	ADJ1610 Mutine TE
154	28	66.7	1514	2	ADJ1608	ADJ1608 Mutine TE
155	28	66.7	1514	2	ADJ1546	ADJ1546 Mutine TE
156	28	66.7	1514	2	ADJ1602	ADJ1602 Mutine TE
157	28	66.7	1514	2	ADJ1612	ADJ1612 Mutine TE
158	28	66.7	1514	2	ADJ1614	ADJ1614 Mutine TE
159	28	66.7	1514	2	ADJ1606	ADJ1606 Mutine TE
160	28	66.7	1514	2	ADJ87520	ADJ87520 Mouse ant
161	28	66.7	1514	2	AAW8122	AAW8122 Murine ma
162	28	66.7	1514	2	AAW8190	AAW8190 Anti-19E
163	28	66.7	1514	2	AAW8184	AAW8184 Anti-19E
164	28	66.7	1514	2	AAW8182	AAW8182 Anti-19E
165	28	66.7	1514	2	AAW8186	AAW8186 Anti-19E
166	28	66.7	1514	2	AAW8188	AAW8188 Anti-19E
167	28	66.7	1514	2	ADJ22421	ADJ22421 Partner d
168	28	66.7	1514	2	ADJ21181	ADJ21181 Domain an
169	28	66.7	1514	2	ADJ36405	ADJ36405 Intracell

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:12 ; Search time 8.26531 Seconds  
(without alignments)  
104.769 Million cell updates/sec

Title: US-10-067-484-2  
Perfect score: 42  
Sequence: 1 PTSPNXXRK 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR 80:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	35	83.3	336	2 T09133	heat shock protein
2	33	78.6	345	2 B43731	achete-scute comp
3	33	78.6	605	2 S18648	protein kinase wls
4	33	78.6	779	1 MMVZAL	ribonucleoside-dip
5	32	76.2	405	2 A75105	hypothetical prote
6	32	76.2	713	2 B91118	probable ferrichro
7	32	76.2	713	2 D85963	probable iron comp
8	31	73.8	127	2 G75086	hypothetical prote
9	31	73.8	372	2 T39649	cell division cont
10	31	73.8	1300	2 T18364	ro-3 protein - Neu
11	31	73.8	1347	2 T41321	BTB domain and Ank
12	30	71.4	307	2 G69501	UDP-glucose 4-epim
13	30	71.4	362	2 A10433	trypsin-like prote
14	30	71.4	371	2 T16391	hypothetical prote
15	30	71.4	399	2 AD2559	hypothetical prote
16	30	71.4	407	2 B81914	probable transmemb
17	30	71.4	414	2 C89428	protein T08D2.7 [l
18	30	71.4	426	2 F81187	glucose/galactose
19	30	71.4	498	2 H97214	endoglucanase, fam
20	30	71.4	529	2 AH0453	bifunctional purin
21	30	71.4	638	2 AE1483	B. subtilis IOD p
22	30	71.4	687	2 D84126	penicillin-binding
23	30	71.4	870	1 GNMVJA	pol polypeptide -
24	30	71.4	1029	2 H86179	hypothetical prote
25	29	69.0	178	2 S51388	hypothetical prote
26	29	69.0	202	2 A86864	conserved hypothet
27	29	69.0	213	2 A87259	hypothetical prote
28	29	69.0	216	2 AH2635	bacteriophage repr
29	29	69.0	216	2 G97417	hypothetical prote

30	29	69.0	256	2 C90443	hypothetical prote
31	29	69.0	374	2 S53829	ribosomal protein
32	29	69.0	389	2 S68175	cone arrestin - bu
33	29	69.0	389	2 S68172	cone arrestin - no
34	29	69.0	470	2 T51196	hypothetical prote
35	29	69.0	480	2 B64308	hypothetical prote
36	29	69.0	494	2 D64944	probable permease
37	29	69.0	494	2 F85794	probable transport
38	29	69.0	494	2 B90946	helicase (EC 3.6.1
39	29	69.0	498	1 HJBE11	neuroilin - goldfif
40	29	69.0	523	2 T50478	conserved hypothet
41	29	69.0	527	2 D87318	regument protein 1
42	29	69.0	743	2 T42557	dynamn-related pr
43	29	69.0	903	2 J80327	dynamn-related pr
44	29	69.0	903	2 T50334	probable RNA-direc
45	29	69.0	1350	2 T10803	hypothetical prote
46	28	66.7	77	2 T14930	occlusion-derived
47	28	66.7	88	2 T30366	Ig kappa chain V-I
48	28	66.7	108	1 K1H0HU	genome polypeptide
49	28	66.7	109	2 S61253	genome polypeptide
50	28	66.7	109	2 S61252	genome polypeptide
51	28	66.7	109	2 S61255	genome polypeptide
52	28	66.7	110	2 S61257	genome polypeptide
53	28	66.7	110	2 S61254	genome polypeptide
54	28	66.7	121	2 S40371	Ig kappa chain - h
55	28	66.7	128	2 PN0445	Ig kappa chain pre
56	28	66.7	137	2 S35916	capaid protein VP1
57	28	66.7	137	2 A95297	hypothetical prote
58	28	66.7	201	2 S75047	drpA protein - Syn
59	28	66.7	202	2 E97130	uncaracterized se
60	28	66.7	203	2 G81700	thymidylate kinase
61	28	66.7	203	2 JCI335	genome polypeptide
62	28	66.7	209	2 JCI329	genome polypeptide
63	28	66.7	209	2 JCI332	genome polypeptide
64	28	66.7	209	2 JCI333	genome polypeptide
65	28	66.7	209	2 JCI331	genome polypeptide
66	28	66.7	209	2 JCI330	genome polypeptide
67	28	66.7	209	2 JCI334	genome polypeptide
68	28	66.7	209	2 JCI328	genome polypeptide
69	28	66.7	213	2 S35917	capaid protein VP1
70	28	66.7	234	2 A03912	genome polypeptide
71	28	66.7	247	2 P00661	outer capsid spike
72	28	66.7	247	2 P00659	outer capsid spike
73	28	66.7	265	2 JH0300	synaptoporin - rat
74	28	66.7	274	1 I52851	NAD(P)H2 dehydroge
75	28	66.7	274	1 A30879	NAD(P)H2 dehydroge
76	28	66.7	274	1 A34162	NAD(P)H2 dehydroge
77	28	66.7	281	1 A57691	NAD(P)H2 dehydroge
78	28	66.7	281	1 VPRRRR	NAD(P)H2 dehydroge
79	28	66.7	299	2 A45720	outer capsid prote
80	28	66.7	309	2 S73869	P35 orf135 - Bomby
81	28	66.7	332	2 A03913	hypothetical prote
82	28	66.7	340	2 A35009	genome polypeptide
83	28	66.7	341	2 G84588	C 3.4.23.42 ethemo
84	28	66.7	342	2 S63654	hypothetical prote
85	28	66.7	354	1 G64648	hypothetical prote
86	28	66.7	354	2 G71938	hypothetical prote
87	28	66.7	359	2 H81421	flagellar motor sw
88	28	66.7	359	2 T01049	flagellar motor sw
89	28	66.7	400	2 T19517	flagellar motor sw
90	28	66.7	409	1 BVBSCB	hypothetical prote
91	28	66.7	428	2 B48836	competence protein
92	28	66.7	428	2 B75133	cytochrome-c3 hydr
93	28	66.7	429	2 C71075	cytochrome-c3 hydr
94	28	66.7	431	2 T02064	probable cytochrom
95	28	66.7	465	2 S61133	histone acetyltran
96	28	66.7	471	2 G75627	hypothetical prote
97	28	66.7	512	2 AB0603	hypothetical prote
98	28	66.7	512	2 B75332	probable ABC trans
99	28	66.7	521	2 T05684	extracellular solu
100	28	66.7	524	2 S55097	hypothetical prote
101	28	66.7	561	2 G90328	probable membrane
102	28	66.7			hypothetical prote



103	28	66.7	584	2	D81265	hypothetical prote
104	28	66.7	585	2	S46034	hypothetical prote
105	28	66.7	609	2	T28896	hypothetical prote
106	28	66.7	614	2	S27662	modulator recognit
107	28	66.7	643	2	A43647	paraportol crystal
108	28	66.7	645	2	A82689	DNA helicase Xf138
109	28	66.7	648	2	A32576	beta-glucuronidase
110	28	66.7	648	2	A25047	beta-glucuronidase
111	28	66.7	733	2	Q01891	capaid protein - 4
112	28	66.7	733	2	Q01892	capaid protein - 4
113	28	66.7	747	2	QRECFE	ferrichrome-iron x
114	28	66.7	747	2	B85499	outer membrane rec
115	28	66.7	747	2	B90648	outer membrane rec
116	28	66.7	776	2	VPXRRI	outer layer protei
117	28	66.7	776	2	A48731	outer layer protei
118	28	66.7	841	2	S69563	suppressor protein
119	28	66.7	961	2	S86245	hypothetical prote
120	28	66.7	993	2	T09129	probable erythrin
121	28	66.7	1011	1	GNNYCI	genome polyprotein
122	28	66.7	1075	2	S54067	probable membrane
123	28	66.7	1643	1	RRWGNV	genome polyprotein
124	28	66.7	1701	2	T09127	probable erythrin
125	28	66.7	1900	2	A02391	serine/histidyl
126	28	66.7	1978	2	S71257	hypothetical prote
127	28	66.7	2014	2	T11560	hypothetical prote
128	28	66.7	2149	2	C96695	ribulose biphosph
129	28	66.7	2332	1	GNNYF	genome polyprotein
130	28	66.7	2336	2	S37077	genome polyprotein
131	28	66.7	2405	2	T81654	transcription fact
132	28	66.7	2539	2	A56923	transcription fact
133	28	66.7	2561	2	T24864	transcription fact
134	28	66.7	2578	2	A56046	transcription fact
135	27	64.3	20	2	A50622	urinary tract ston
136	27	64.3	115	2	T40624	hypothetical prote
137	27	64.3	115	2	C81142	pmk protein NMB09
138	27	64.3	142	1	S47821	phf protein - Sac
139	27	64.3	142	1	S47821	interleukin-3 prec
140	27	64.3	219	2	H17585	hydrogenase expres
141	27	64.3	219	2	S12424	YOGF protein - Yea
142	27	64.3	219	2	S03766	targeted effector
143	27	64.3	222	2	H90730	virulence protein
144	27	64.3	229	1	H61098	hypothetical membr
145	27	64.3	233	2	D51066	probable pyridoxam
146	27	64.3	233	2	D51066	hypothetical membr
147	27	64.3	247	2	D85910	unknown protein en
148	27	64.3	252	2	T15977	pectinesterase (EC
149	27	64.3	274	2	H83868	conserved hypothe
150	27	64.3	276	2	T06817	conserved hypothe
151	27	64.3	291	2	G80634	hypothetical prote
152	27	64.3	312	2	S79525	pectinesterase (EC
153	27	64.3	312	2	S79525	pectinesterase (EC
154	27	64.3	314	2	T16272	pectinesterase (EC
155	27	64.3	315	2	T16272	pectinesterase (EC
156	27	64.3	315	2	S51875	phock protein - Rhi
157	27	64.3	317	2	S74735	phosphate acetyltr
158	27	64.3	320	2	S74735	pectinesterase (EC
159	27	64.3	320	2	S74735	pectinesterase (EC
160	27	64.3	324	2	R43649	aviluncine protein
161	27	64.3	324	2	R43649	hypothetical prote
162	27	64.3	324	2	R81183	probable methylst
163	27	64.3	335	2	T30538	heat shock protein
164	27	64.3	335	2	AD1052	hypothetical prote
165	27	64.3	338	2	H98233	hypothetical prote
166	27	64.3	358	2	H97144	ferrichrome-bindin
167	27	64.3	358	1	WCPVND	coat protein Vp1 -
168	27	64.3	367	2	A81367	probable GTP-bind
169	27	64.3	368	2	C29356	hydroxyproline-ric
170	27	64.3	373	2	R49094	methoxymalonyl-CoA
171	27	64.3	385	2	B81725	hypothetical prote
172	27	64.3	394	2	S50486	hypothetical prote
173	27	64.3	398	2	AR2769	hypothetical prote
174	27	64.3	410	2	T45848	hypothetical prote
175	27	64.3	412	1	G69965	ATP/GTP-binding pr
176	27	64.3	418	2	A81394	Probable sugar tra
177	27	64.3	420	2	F97549	glutathione-indupe
178	27	64.3	423	2	S51369	chitinase i fungus
179	27	64.3	424	2	S68121	chitinase i fungus
180	27	64.3	428	2	AF0302	Probable solute
181	27	64.3	432	2	C95275	Probable ABC trans
182	27	64.3	436	2	T43197	nucleoporin
183	27	64.3	436	2	T36478	Probable solute-bi
184	27	64.3	445	2	D70179	Na+/H+-exchanging
185	27	64.3	455	2	H97237	membrane associat
186	27	64.3	469	2	T00429	Probable pectinest
187	27	64.3	472	2	A60330	peptidase M20/M25
188	27	64.3	474	2	B87650	unknown protein P1
189	27	64.3	509	2	D67994	ribosome transport
190	27	64.3	510	2	A84887	ribosome transport
191	27	64.3	514	2	A83563	catalse (EC 1.11.
192	27	64.3	536	2	B75329	Probable zinc fing
193	27	64.3	547	2	T41213	Probable NLI prote
194	27	64.3	552	2	S42253	Probable pectinest
195	27	64.3	554	2	T06374	pectinesterase (EC
196	27	64.3	554	2	T06468	pectinesterase (EC
197	27	64.3	559	2	A46462	Probable pectinest
198	27	64.3	570	2	T46261	hypothetical prote
199	27	64.3	573	2	T01317	hypothetical prote
200	27	64.3	579	2	B86158	hypothetical prote
201	27	64.3	589	2	AD2263	hypothetical prote
202	27	64.3	595	2	AF2097	hypothetical prote
203	27	64.3	619	2	T26453	probable protein X
204	27	64.3	634	2	S20138	Sac7 protein - yea
205	27	64.3	654	2	S63672	hypothetical prote
206	27	64.3	661	2	AG3422	Probable zinc fing
207	27	64.3	684	2	T41385	v-type ATP synthas
208	27	64.3	690	2	T72197	hypothetical prote
209	27	64.3	697	2	T12127	hypothetical prote
210	27	64.3	700	2	S63580	stomatocin beta c
211	27	64.3	710	2	WY2844	cyclonucleoside-dip
212	27	64.3	711	1	WY2844	ribonucleoside-dip
213	27	64.3	771	2	B26845	ribonucleoside-dip
214	27	64.3	771	2	B26845	ribonucleoside-dip
215	27	64.3	771	2	B26845	ribonucleoside-dip
216	27	64.3	771	2	B26845	ribonucleoside-dip
217	27	64.3	776	1	WY2844	outer layer protei
218	27	64.3	776	1	WY2844	outer layer protei
219	27	64.3	779	2	S56345	cell division cont
220	27	64.3	786	1	S24050	ribonucleoside-dip
221	27	64.3	792	2	B16480	ribonucleoside-dip
222	27	64.3	792	2	B16480	ribonucleoside-dip
223	27	64.3	795	2	B46687	hypothetical prote
224	27	64.3	804	2	S34807	ribonucleoside-dip
225	27	64.3	811	2	S62577	ribonucleoside-dip
226	27	64.3	811	2	S62577	ribonucleoside-dip
227	27	64.3	816	2	B84605	hypothetical prote
228	27	64.3	817	2	T22442	hypothetical prote
229	27	64.3	821	2	AD1507	probable secreted
230	27	64.3	821	2	AD1507	probable secreted
231	27	64.3	841	2	A49412	ribonucleoside-dip
232	27	64.3	851	2	T00374	hypothetical prote
233	27	64.3	856	2	P87316	conserved hypotet
234	27	64.3	885	1	WMBY31	ribonucleoside-dip
235	27	64.3	888	2	S50573	ribonucleoside-dip
236	27	64.3	893	2	B50573	ribonucleoside-dip
237	27	64.3	929	2	T43711	cell wall surface
238	27	64.3	929	2	B83502	ribonucleoside-dip
239	27	64.3	963	2	B83502	ribonucleoside-dip
240	27	64.3	966	2	D96662	ribonucleoside-dip
241	27	64.3	1025	2	S69790	fibronectin-bindin
242	27	64.3	1028	2	F87584	Tomb-dependent rec
243	27	64.3	1063	2	E96662	hypothetical prote
244	27	64.3	1063	2	E96662	hypothetical prote
245	27	64.3	1237	2	S64385	probable membrane
246	27	64.3	1251	2	T21389	hypothetical prote
247	27	64.3	1289	2	S69689	hypothetical prote
248	27	64.3	1298	2	I54367	X-linked nuclear p

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:05 ; Search time 49.0408 Seconds  
(without alignments)  
129.479 Million cell updates/sec

Title: US-10-067-484-2  
Perfect score: 42  
Sequence: 1 PTFXKARK 9

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Uniprot 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	83.3	336	076224	GYRYP
2	35	83.3	492	081NH2	BACAN
3	34	81.0	398	082MK5	PYRAE
4	34	81.0	434	0893V9	CLOTE
5	33	78.6	178	060Y71	CABER
6	33	78.6	242	08KDZ1	CHLRE
7	33	78.6	250	0517R9	ENTHI
8	33	78.6	271	0941A9	ARATH
9	33	78.6	336	077029	DROYA
10	33	78.6	345	1AST4	DROME
11	33	78.6	345	04V705	DROME
12	33	78.6	346	077031	DROSI
13	33	78.6	460	06C3D8	YARLI
14	33	78.6	468	0758Z1	ASHGO
15	33	78.6	605	1WIS1	SCHPO
16	33	78.6	778	1RIR1	ASFB7
17	33	78.6	779	1RIR1	ASFB7
18	33	78.6	901	06CAJ2	YARLI
19	33	78.6	1041	06XST7	STRSU
20	32	76.2	104	05Z7J8	ORISA
21	32	76.2	185	09A7B9	ORISA
22	32	76.2	311	05FNU5	GLUXO
23	32	76.2	320	054QD9	DICDI
24	32	76.2	388	07RGP9	PIAYO
25	32	76.2	405	04XW08	PIACH
26	32	76.2	459	09UZB7	PYRAB
27	32	76.2	459	05LDS1	BACFN
28	32	76.2	459	064U70	BACFR
29	32	76.2	492	04Z327	PIABE
30	32	76.2	492	04MXD6	BACCE
31	32	76.2	492	0735B2	BACCL

32	32	76.2	492	2	06HGM1	BACHK
33	32	76.2	492	2	0639A8	BACCZ
34	32	76.2	521	2	04LINO	YBURK
35	32	76.2	713	2	08PDI8	ECOL6
36	32	76.2	713	2	08XB05	ECOS7
37	32	76.2	808	2	09UK68	HUMAN
38	32	76.2	844	2	06P517	HUMAN
39	32	76.2	881	2	05RBE3	PONPY
40	32	76.2	891	2	04UBQ2	THEAN
41	32	76.2	897	2	06FL60	CANGA
42	32	76.2	1378	2	0584U4	GYRYP
43	32	76.2	1434	2	08LJ13	PLAF7
44	32	76.2	1636	2	04TBC0	TESTG
45	32	76.2	1646	2	05CFZ6	CRYHO
46	32	76.2	1940	2	07SAX4	NEUCR
47	32	76.2	2829	1	APC	XENLA
48	32	76.2	3347	2	08MJJ9	BOMMO
49	32	76.2	3354	2	08T101	BOMMO
50	31	73.8	88	2	08JUI4	9PIC0
51	31	73.8	124	2	0949J0	CUCSA
52	31	73.8	127	2	09UZR0	PYRAB
53	31	73.8	130	2	04ZWH5	PESBY
54	31	73.8	130	2	04LHB8	PESBH
55	31	73.8	133	2	06FUC2	ANOGA
56	31	73.8	135	2	08BCV7	PSEBP
57	31	73.8	156	2	06F173	MESFL
58	31	73.8	190	2	05D015	9PFLI
59	31	73.8	193	2	05D019	9PFLI
60	31	73.8	195	2	05D008	9PFLI
61	31	73.8	195	2	0952X8	9PULM
62	31	73.8	211	2	0952Y4	9PULM
63	31	73.8	211	2	0952Y3	9PULM
64	31	73.8	211	2	0952X5	9PULM
65	31	73.8	221	2	0872B6	NEUCR
66	31	73.8	241	2	06UHA0	CABER
67	31	73.8	252	2	0526U8	MAGGR
68	31	73.8	262	2	08DLX3	SYNEL
69	31	73.8	267	2	07VUP4	HEILHP
70	31	73.8	287	2	051B19	ENTHI
71	31	73.8	294	2	0981B7	RHTLO
72	31	73.8	310	2	06D9X6	ERRCT
73	31	73.8	359	2	08XIV3	CLOPE
74	31	73.8	372	1	DPD03	SCHPO
75	31	73.8	388	2	08A308	BACTN
76	31	73.8	397	2	08TFB0	TRIVE
77	31	73.8	425	2	0524G8	MAGGR
78	31	73.8	457	2	09VGU7	DROME
79	31	73.8	474	2	07PZT6	ANOGA
80	31	73.8	498	2	09FT67	ARATH
81	31	73.8	525	2	05XEP8	ARATH
82	31	73.8	525	2	08LPJ6	ARATH
83	31	73.8	540	2	04VBB5	RAT
84	31	73.8	633	2	06CHX2	YARLI
85	31	73.8	658	2	04KFL8	PSEF5
86	31	73.8	726	2	051C30	ENTHI
87	31	73.8	790	2	0891X1	CLOTE
88	31	73.8	791	2	06CH93	YARLI
89	31	73.8	1130	2	08EMH7	MYCPE
90	31	73.8	1300	1	DYNA	NEUCR
91	31	73.8	1328	2	064XZ1	BACFR
92	31	73.8	1427	2	0748B1	SCHPO
93	31	73.8	1347	2	05LH34	BACFN
94	31	73.8	1504	2	051TP6	MAGGR
95	31	73.8	1561	2	054V07	DICDI
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97	31	73.8	1836	2	04QBB2	LEITWA
98	31	73.8	16215	2	09NFS3	DROME
99	31	73.8	17903	2	07RTL4	DROME
100	31	73.8	18074	2	091TU4	DROME
101	30.5	72.6	45	2	091HS1	9PIC0
102	30.5	72.6	55	2	09DSB0	9PIC0
103	30.5	72.6	77	2	091H65	9PIC0
104	30.5	72.6	81	2	091H50	9PIC0

06Hgm1 bacillus th  
0639a8 bacillus ce  
04Lino burkholderi  
08PDI8 escherichia  
08XB05 escherichia  
09UK68 homo sapien  
06P517 homo sapien  
05RBE3 pongo pygma  
04UBQ2 theileria a  
06FL60 candida gla  
0584U4 trypanosoma  
08LJ13 plasmodium  
04TBC0 tetraodon n  
05CFZ6 cryptospori  
07SAX4 neuropepti  
P70039 xenopus lae  
08mjj9 bombay mori  
08T101 bombay mori  
08JUI4 foot-and-mo  
0949J0 cucumis sat  
09UZR0 pseudomonas  
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04LHB8 pseudomonas  
06FUC2 anopheles g  
08BCV7 pseudomonas  
06F173 mesoplasma  
05D015 asplenium o  
05D019 asplenium t  
05D008 asplenium t  
0952X8 patula tae  
0952Y4 patula moo  
0952Y3 patula moo  
0952X5 patula loh  
0872B6 neurospora  
06UHA0 caenorhabdi  
0526U8 magnaporthe  
08DLX3 synechococc  
07VUP4 helicobacte  
051B19 entamoeba h  
0981B7 rhizobium l  
06D9X6 erynia car  
08XIV3 clostridium  
P30261 schizosacch  
08A308 bacteroides  
08TFB0 trichoderma  
0524G8 magnaporthe  
09VGU7 drosophila  
07PZT6 anopheles g  
09FT67 arabidopsis  
05XEP8 arabidopsis  
08LPJ6 arabidopsis  
04VBB5 rattus norv  
06CHX2 yarrowia li  
04KFL8 pseudomonas  
051C30 entamoeba h  
0891X1 clostridium  
06CH93 yarrowia li  
08EMH7 mycoplasma  
001397 neurospora  
064XZ1 bacteroides  
0748B1 schizosacch  
05LH34 bacteroides  
051TP6 magnaporthe  
054V07 dictyostell  
04MHH4 aspergillus  
04QBB2 leishmania  
09NFS3 drosophila  
07RTL4 drosophila  
091TU4 drosophila  
091HS1 foot-and-mo  
09DSB0 foot-and-mo  
091H65 foot-and-mo  
091H50 foot-and-mo

[illegible]

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:21 ; Search time 17.449 Seconds  
(without alignments)  
42.643 Million cell updates/sec

Title: US-10-067-484-2  
Perfect score: 42  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/prodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/PC/US\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/RC\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	32	76.2	232 2	US-09-489-039A-7297 Sequence 7297, Ap
2	30	71.4	100 2	US-09-198-452A-502 Sequence 502, App
3	30	71.4	154 2	US-09-489-039A-15010 Sequence 12010, A
4	30	71.4	214 2	US-09-134-000C-4529 Sequence 4529, Ap
5	30	71.4	287 2	US-09-352-991A-23091 Sequence 23091, A
6	30	71.4	441 2	US-09-328-352-6369 Sequence 6369, Ap
7	30	71.4	987 2	US-09-540-236-3017 Sequence 3017, Ap
8	30	71.4	1380 2	US-09-328-352-8132 Sequence 8132, Ap
9	30	71.4	2626 2	US-09-477-962-106 Sequence 106, App
10	29	69.0	92 2	US-09-248-796A-17403 Sequence 17403, A
11	29	69.0	106 1	US-08-800-198-4 Sequence 4, Appl1
12	29	69.0	106 2	US-09-296-595-4 Sequence 4, Appl1
13	29	69.0	231 2	US-09-248-796A-15529 Sequence 15529, A
14	29	69.0	239 1	US-07-956-399-4 Sequence 4, Appl1
15	29	69.0	240 1	US-08-800-198-8 Sequence 8, Appl1
16	29	69.0	240 2	US-09-296-595-8 Sequence 8, Appl1
17	29	69.0	252 2	US-09-328-352-6267 Sequence 6267, Ap
18	29	69.0	302 2	US-09-248-796A-14926 Sequence 14926, A
19	29	69.0	340 1	US-09-134-001C-5182 Sequence 5182, Ap
20	29	69.0	466 1	US-08-432-016-4 Sequence 4, Appl1
21	29	69.0	466 2	US-08-684-594-4 Sequence 4, Appl1
22	29	69.0	756 2	US-09-248-796A-19209 Sequence 19209, A
23	29	69.0	785 2	US-09-302-540-10007 Sequence 10007, A
24	29	69.0	935 2	US-09-134-000C-6493 Sequence 6493, Ap
25	29	69.0	1514 1	US-08-853-310-4 Sequence 4, Appl1
26	28	66.7	34 2	US-09-100-600A-6 Sequence 6, Appl1
27	28	66.7	34 2	US-09-100-600A-7 Sequence 7, Appl1

28	66.7	34	2	US-09-100-600A-12 Sequence 12, Appl
29	66.7	34	2	US-09-100-600A-13 Sequence 13, Appl
30	66.7	34	2	US-09-100-600A-20 Sequence 20, Appl
31	66.7	34	2	US-09-100-600A-21 Sequence 21, Appl
32	66.7	36	2	US-09-100-600A-4 Sequence 4, Appl1
33	66.7	36	2	US-09-100-600A-5 Sequence 5, Appl1
34	66.7	36	2	US-09-100-600A-10 Sequence 10, Appl
35	66.7	36	2	US-09-100-600A-11 Sequence 11, Appl
36	66.7	45	2	US-09-100-600A-87 Sequence 87, Appl
37	66.7	45	2	US-09-100-600A-88 Sequence 88, Appl
38	66.7	45	2	US-09-100-600A-89 Sequence 89, Appl
39	66.7	45	2	US-09-100-600A-90 Sequence 90, Appl
40	66.7	45	2	US-09-100-600A-91 Sequence 91, Appl
41	66.7	46	2	US-09-100-600A-71 Sequence 41, Appl
42	66.7	46	2	US-09-270-767-37739 Sequence 37739, A
43	66.7	46	2	US-09-270-767-52956 Sequence 52956, A
44	66.7	47	2	US-09-100-600A-67 Sequence 67, Appl
45	66.7	47	2	US-09-100-600A-68 Sequence 68, Appl
46	66.7	47	2	US-09-100-600A-70 Sequence 70, Appl
47	66.7	47	2	US-09-100-600A-71 Sequence 71, Appl
48	66.7	47	2	US-09-100-600A-72 Sequence 72, Appl
49	66.7	47	2	US-09-100-600A-73 Sequence 73, Appl
50	66.7	47	2	US-09-100-600A-74 Sequence 74, Appl
51	66.7	47	2	US-09-100-600A-75 Sequence 75, Appl
52	66.7	47	2	US-09-100-600A-76 Sequence 76, Appl
53	66.7	47	2	US-09-100-600A-77 Sequence 77, Appl
54	66.7	47	2	US-09-100-600A-78 Sequence 78, Appl
55	66.7	47	2	US-09-100-600A-80 Sequence 80, Appl
56	66.7	47	2	US-09-100-600A-81 Sequence 81, Appl
57	66.7	47	2	US-09-100-600A-82 Sequence 82, Appl
58	66.7	47	2	US-09-100-600A-83 Sequence 83, Appl
59	66.7	47	2	US-09-100-600A-84 Sequence 84, Appl
60	66.7	47	2	US-09-100-600A-85 Sequence 85, Appl
61	66.7	47	2	US-09-100-600A-86 Sequence 86, Appl
62	66.7	56	2	US-09-100-414B-103 Sequence 103, App
63	66.7	56	2	US-09-100-600A-31 Sequence 31, Appl
64	66.7	56	2	US-09-303-323-103 Sequence 103, App
65	66.7	56	2	US-09-770-014-103 Sequence 103, App
66	66.7	56	2	US-09-770-014-103 Sequence 103, App
67	66.7	64	2	US-09-701-588C-101 Sequence 101, App
68	66.7	64	2	US-09-248-796A-28206 Sequence 28206, A
69	66.7	72	2	US-09-100-414B-104 Sequence 104, App
70	66.7	72	2	US-09-100-600A-32 Sequence 32, Appl
71	66.7	72	2	US-09-303-323-104 Sequence 104, App
72	66.7	72	2	US-09-770-014-104 Sequence 104, App
73	66.7	72	2	US-09-701-588C-102 Sequence 102, App
74	66.7	77	2	US-09-270-767-36631 Sequence 36631, A
75	66.7	77	2	US-09-270-767-51848 Sequence 51848, A
76	66.7	80	2	US-09-100-600A-30 Sequence 30, Appl
77	66.7	86	2	US-09-248-796A-21594 Sequence 21594, A
78	66.7	91	2	US-09-248-796A-21573 Sequence 21573, A
79	66.7	100	2	US-09-127-721A-4 Sequence 4, Appl1
80	66.7	107	2	US-08-476-176B-4 Sequence 4, Appl1
81	66.7	107	2	US-08-485-246A-4 Sequence 4, Appl1
82	66.7	107	2	US-09-270-767-37482 Sequence 37482, A
83	66.7	120	2	US-09-270-767-52699 Sequence 52699, A
84	66.7	120	2	US-09-248-796A-24518 Sequence 24518, A
85	66.7	127	1	US-08-476-176B-6 Sequence 6, Appl1
86	66.7	127	1	US-08-476-176B-8 Sequence 8, Appl1
87	66.7	127	1	US-08-476-176B-10 Sequence 10, Appl1
88	66.7	127	1	US-08-127-721A-6 Sequence 6, Appl1
89	66.7	127	2	US-08-127-721A-8 Sequence 8, Appl1
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92	66.7	127	2	US-08-485-246A-8 Sequence 8, Appl1
93	66.7	127	2	US-08-485-246A-10 Sequence 10, Appl1
94	66.7	137	2	US-09-489-039A-1167 Sequence 1167, A
95	66.7	139	2	US-09-252-991A-28981 Sequence 28981, A
96	66.7	175	2	US-09-134-000C-6776 Sequence 6776, Ap
97	66.7	219	2	US-09-370-767-60584 Sequence 60584, A
98	66.7	240	1	US-07-956-399-2 Sequence 2, Appl1
99	66.7	243	2	US-09-270-767-45088 Sequence 45088, A
100	66.7	244	2	US-09-244-369B-1 Sequence 1, Appl1

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101	28	66.7	244	2	US-09-270-767-22411	Sequence 62411, A	175	27	64.3	779	2	US-08-477-346-32	Sequence 32, Appl
102	28	66.7	244	2	US-09-248-796A-18676	Sequence 18676, A	176	27	64.3	779	2	US-08-487-089-32	Sequence 32, Appl
103	28	66.7	244	2	US-09-270-767-19892	Sequence 3892, A	177	27	64.3	779	2	US-09-178-052A-25	Sequence 29, Appl
104	28	66.7	244	2	US-09-270-767-55109	Sequence 55109, A	178	27	64.3	779	2	US-09-328-016-6015	Sequence 6015, App
105	28	66.7	452	2	US-09-540-236-3030	Sequence 3030, App	179	27	64.3	792	2	US-09-270-767-45282	Sequence 45282, A
106	28	66.7	501	2	US-09-502-540-10047	Sequence 10047, A	180	27	64.3	800	2	US-08-949-016-11342	Sequence 11342, A
107	28	66.7	507	2	US-09-770-767-46787	Sequence 46787, A	181	27	64.3	808	2	US-08-136-743B-4	Sequence 4, Appl
108	28	66.7	524	2	US-09-242-913B-15	Sequence 15, Appl	182	27	64.3	811	1	US-09-769-787-126	Sequence 16, App
109	28	66.7	524	2	US-09-442-913B-15	Sequence 11958, A	183	27	64.3	916	2	US-09-902-540-10793	Sequence 10793, A
110	28	66.7	528	2	US-09-489-039A-11958	Sequence 4323, Ap	184	27	64.3	919	2	US-10-101-464A-642	Sequence 642, App
111	28	66.7	541	2	US-09-543-681A-4323	Sequence 2497, Ap	185	27	64.3	950	2	US-09-328-352-4668	Sequence 4668, App
112	28	66.7	619	2	US-10-104-047-2497	Sequence 7, Appl	186	27	64.3	950	2	US-09-252-991A-19450	Sequence 19450, App
113	28	66.7	644	2	US-08-793-331-7	Sequence 4, Appl	187	27	64.3	998	2	US-10-101-464A-809	Sequence 809, App
114	28	66.7	724	2	US-09-715-855-4	Sequence 6, Appl	188	27	64.3	1333	2	US-09-808-701A-25	Sequence 25, App
115	28	66.7	725	2	US-08-793-331-4	Sequence 18, Appl	189	27	64.3	1381	2	US-08-169-927-2	Sequence 2, Appl
116	28	66.7	776	1	US-07-603-323-6	Sequence 14987, A	190	27	64.3	1612	2	US-09-538-092-1131	Sequence 1131, Ap
117	28	66.7	936	2	US-08-248-796B-14987	Sequence 5, Appl	191	27	64.3	1792	2	US-09-959-897-42	Sequence 42, Appl
118	28	66.7	1183	2	US-08-929-329-5	Sequence 24, Appl	192	27	64.3	5179	2	US-09-959-897-42	Sequence 24, Appl
119	28	66.7	1507	2	US-08-929-329-5	Sequence 24, Appl	193	27	64.3	42	2	US-09-248-796A-24588	Sequence 24588, A
120	28	66.7	2318	2	US-09-091-319-24	Sequence 24, Appl	194	27	64.3	88	2	US-09-248-796A-25011	Sequence 25011, A
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122	28	66.7	2318	1	US-08-821-555A-7	Sequence 7, Appl	196	26	61.9	108	2	US-09-248-796A-25175	Sequence 2, Appl
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124	28	66.7	2973	2	US-09-136-605-7	Sequence 88, Appl	198	26	61.9	137	2	US-09-248-796A-25175	Sequence 8, Appl
125	28	66.7	41	2	US-08-836-61A-88	Sequence 84, Appl	199	26	61.9	137	2	US-09-248-796A-25175	Sequence 8, Appl
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129	27	64.3	86	2	US-09-543-681A-6348	Sequence 6348, Ap	203	26	61.9	147	1	US-09-270-767-40153	Sequence 40153, A
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86.753 Million cell updates/sec

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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5	33	78.6	101	4	US-10-437-963-158168
6	33	78.6	345	6	US-11-097-143-7386
7	33	78.6	1179	4	US-10-437-963-167415
8	32	76.2	51	4	US-10-425-115-298537
9	32	76.2	148	4	US-10-767-701-48958
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11	32	76.2	179	4	US-10-437-963-192813
12	32	76.2	436	4	US-10-437-963-159333
13	32	76.2	713	4	US-10-238-075-263
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31	30	71.4	109	4	US-10-424-599-194644	Sequence 194644,
32	30	71.4	116	4	US-10-425-115-256410	Sequence 256410,
33	30	71.4	187	5	US-10-450-763-35325	Sequence 35325, A
34	30	71.4	371	4	US-10-369-493-6753	Sequence 6753, Ap
35	30	71.4	407	4	US-10-282-122A-65777	Sequence 65777, A
36	30	71.4	418	4	US-10-362-881-31	Sequence 31, Appl
37	30	71.4	426	4	US-10-282-122A-65458	Sequence 65458, A
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39	30	71.4	1363	4	US-10-424-599-151501	Sequence 63099, A
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47	29	69.0	108	4	US-10-424-599-203533	Sequence 203533,
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50	29	69.0	116	4	US-10-767-701-37364	Sequence 37364, A
51	29	69.0	127	4	US-10-374-600-5	Sequence 5, Appl
52	29	69.0	127	4	US-10-374-600-11	Sequence 11, Appl
53	29	69.0	127	4	US-10-374-600-15	Sequence 15, Appl
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61	29	69.0	233	4	US-10-282-122A-71928	Sequence 71928, A
62	29	69.0	236	5	US-10-728-722-18	Sequence 18, Appl
63	29	69.0	296	4	US-10-425-115-51353	Sequence 51353, A
64	29	69.0	340	4	US-10-724-972A-4184	Sequence 4184, Ap
65	29	69.0	413	4	US-10-282-122A-50763	Sequence 50763, A
66	29	69.0	417	4	US-10-259-1942A-212	Sequence 212, App
67	29	69.0	473	4	US-10-156-761-7722	Sequence 7722, Ap
68	29	69.0	487	3	US-09-748-875-9	Sequence 9, Appl
69	29	69.0	487	3	US-09-748-875-66	Sequence 66, Appl
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73	29	69.0	487	5	US-10-341-201-9	Sequence 9, Appl
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75	29	69.0	494	3	US-09-741-66B-468	Sequence 468, App
76	29	69.0	494	4	US-10-282-122A-42683	Sequence 42683, A
77	29	69.0	498	5	US-10-491-653-146	Sequence 146, App
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80	29	69.0	754	4	US-10-369-493-8297	Sequence 8297, Ap
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82	29	69.0	786	4	US-10-437-963-158130	Sequence 158130,
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84	29	69.0	913	4	US-10-369-493-7255	Sequence 7255, Ap
85	29	69.0	924	4	US-10-369-493-4496	Sequence 4496, Ap
86	29	69.0	1001	4	US-10-369-493-8610	Sequence 8610, Ap
87	29	69.0	1042	4	US-10-282-122A-46603	Sequence 46603, A
88	29	69.0	1060	5	US-10-732-922A-50061	Sequence 50061, A
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91	29	69.0	1172	6	US-11-097-143-26190	Sequence 26190, A
92	28	66.7	11	5	US-10-946-647-745	Sequence 745, App
93	28	66.7	12	4	US-10-012-363A-5	Sequence 5, Appl
94	28	66.7	42	4	US-10-425-115-351241	Sequence 351241,
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98	28	66.7	61	4	US-10-425-115-321847	Sequence 321847,
99	28	66.7	65	4	US-10-355-161A-11	Sequence 13, Appl
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102	28	66.7	79	4	US-10-425-115-361796	Sequence 361796,	175	28	66.7	265	5	US-10-737-450-8	Sequence 8, App
103	28	66.7	80	4	US-10-425-114-41588	Sequence 41588, A	176	28	66.7	294	5	US-10-051-874-111	Sequence 111, App
104	28	66.7	80	4	US-10-425-115-350274	Sequence 350274,	177	28	66.7	285	4	US-10-087-684-59	Sequence 59, App
105	28	66.7	81	4	US-10-437-963-171355	Sequence 171355,	178	28	66.7	295	4	US-10-218-779-59	Sequence 59, App
106	28	66.7	82	4	US-09-989-890-205	Sequence 205, App	179	28	66.7	296	3	US-09-825-101-1383	Sequence 1383, App
107	28	66.7	84	4	US-10-425-114-56526	Sequence 56526, A	180	28	66.7	296	4	US-10-282-122A-48567	Sequence 48567, A
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110	28	66.7	96	3	US-09-833-245-943	Sequence 943, App	183	28	66.7	324	3	US-09-764-864-1265	Sequence 1265, App
111	28	66.7	96	3	US-09-833-245-944	Sequence 944, App	184	28	66.7	324	5	US-10-629-950-20	Sequence 20, App
112	28	66.7	97	4	US-10-424-599-169804	Sequence 169804,	185	28	66.7	336	4	US-10-424-599-252619	Sequence 252619,
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114	28	66.7	100	4	US-10-425-114-68308	Sequence 68308, A	187	28	66.7	344	4	US-10-424-599-246855	Sequence 246855,
115	28	66.7	106	4	US-10-453-698-27	Sequence 27, App	188	28	66.7	347	4	US-10-029-386-32228	Sequence 32228, A
116	28	66.7	106	4	US-10-453-698-27	Sequence 27, App	189	28	66.7	349	5	US-10-739-930-8752	Sequence 8752, App
117	28	66.7	107	3	US-09-991-470-25	Sequence 25, App	190	28	66.7	351	4	US-10-425-115-364383	Sequence 364383,
118	28	66.7	107	3	US-10-308-817-129	Sequence 129, App	191	28	66.7	351	4	US-10-084-749-2300	Sequence 2300, App
119	28	66.7	107	4	US-10-308-817-130	Sequence 130, App	192	28	66.7	352	4	US-10-335-977-4796	Sequence 4796, App
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121	28	66.7	107	4	US-10-374-531-11761	Sequence 114, App	194	28	66.7	355	5	US-10-831-070-42	Sequence 42, App
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129	28	66.7	107	5	US-10-901-736-63	Sequence 63, App	202	28	66.7	384	4	US-10-291-265-805	Sequence 805, App
130	28	66.7	107	5	US-10-901-736-65	Sequence 65, App	203	28	66.7	384	4	US-10-291-265-806	Sequence 806, App
131	28	66.7	107	5	US-10-901-736-66	Sequence 65, App	204	28	66.7	384	4	US-10-291-265-807	Sequence 807, App
132	28	66.7	107	5	US-10-901-736-69	Sequence 69, App	205	28	66.7	384	4	US-10-425-115-364382	Sequence 364382,
133	28	66.7	108	4	US-10-425-115-211472	Sequence 211472,	206	28	66.7	385	4	US-10-325-066A-990	Sequence 990, App
134	28	66.7	113	4	US-10-374-600-22	Sequence 22, App	207	28	66.7	387	5	US-10-374-780A-2862	Sequence 2862, App
135	28	66.7	113	4	US-10-374-600-23	Sequence 23, App	208	28	66.7	387	5	US-10-739-930-6133	Sequence 6132, App
136	28	66.7	113	4	US-10-374-531-22	Sequence 23, App	209	28	66.7	387	5	US-10-325-066A-990	Sequence 990, App
137	28	66.7	113	4	US-10-374-531-23	Sequence 23, App	210	28	66.7	387	5	US-10-411-910A-180	Sequence 180, App
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139	28	66.7	113	4	US-10-468-96-2012	Sequence 2012, App	212	28	66.7	420	4	US-10-282-122A-46660	Sequence 46660, A
140	28	66.7	113	4	US-10-450-763-49425	Sequence 49425, A	213	28	66.7	420	4	US-10-365-493-21914	Sequence 21914, A
141	28	66.7	124	4	US-10-767-701-58442	Sequence 58442, A	214	28	66.7	490	4	US-10-437-963-189793	Sequence 189793,
142	28	66.7	127	4	US-10-374-600-17	Sequence 17, App	215	28	66.7	524	4	US-10-425-114-45547	Sequence 45547, A
143	28	66.7	127	4	US-10-374-531-17	Sequence 17, App	216	28	66.7	524	4	US-10-156-761-11398	Sequence 11398,
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145	28	66.7	131	3	US-09-738-626-5204	Sequence 5204, App	218	28	66.7	524	4	US-10-347-278-15	Sequence 15, App
146	28	66.7	134	4	US-10-767-701-5788	Sequence 5788, A	219	28	66.7	524	4	US-11-097-143-41691	Sequence 41691, A
147	28	66.7	144	4	US-10-450-763-34153	Sequence 34153, A	220	28	66.7	524	6	US-10-369-493-12426	Sequence 12426, A
148	28	66.7	155	4	US-10-424-599-205115	Sequence 205115,	221	28	66.7	528	4	US-10-425-115-364387	Sequence 364387,
149	28	66.7	155	4	US-10-437-963-135105	Sequence 135105,	222	28	66.7	528	4	US-10-425-115-314242	Sequence 314242,
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151	28	66.7	188	4	US-10-282-122A-72584	Sequence 72584, A	224	28	66.7	528	4	US-09-890-811A-10	Sequence 10, App
152	28	66.7	191	4	US-10-282-122A-46185	Sequence 46185, A	225	28	66.7	528	4	US-10-450-763-48218	Sequence 48218, App
153	28	66.7	191	4	US-10-282-122A-46896	Sequence 46896, A	226	28	66.7	528	4	US-10-450-763-48247	Sequence 48247, A
154	28	66.7	200	4	US-10-364-397-19	Sequence 19, App	227	28	66.7	528	4	US-10-369-493-3100	Sequence 3100, App
155	28	66.7	203	4	US-10-282-122A-55176	Sequence 55176, A	228	28	66.7	602	4	US-10-146-447-45	Sequence 45, App
156	28	66.7	213	5	US-10-921-741-7	Sequence 7, App	229	28	66.7	614	4	US-10-370-715B-210	Sequence 210, App
157	28	66.7	214	6	US-10-813-483-3	Sequence 3, App	230	28	66.7	614	4	US-10-104-047-2497	Sequence 2497, App
158	28	66.7	214	6	US-11-013-966-3	Sequence 3, App	231	28	66.7	614	4	US-10-425-115-227439	Sequence 227439,
159	28	66.7	215	5	US-10-863-637-9	Sequence 9, App	232	28	66.7	614	4	US-10-421-175-4	Sequence 13, App
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161	28	66.7	218	4	US-10-424-599-255050	Sequence 255050,	234	28	66.7	648	5	US-10-757-093-14	Sequence 14, App
162	28	66.7	222	5	US-10-425-115-364389	Sequence 364389,	235	28	66.7	648	5	US-10-732-923-15070	Sequence 15070, A
163	28	66.7	233	5	US-10-449-531-2	Sequence 53129, A	236	28	66.7	648	5	US-10-425-115-364381	Sequence 364381,
164	28	66.7	235	5	US-10-863-637-1	Sequence 2, App	237	28	66.7	657	6	US-10-732-923-15071	Sequence 15071, A
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171	28	66.7	245	5	US-09-991-470-27	Sequence 27, App	244	28	66.7	751	4	US-10-437-963-189139	Sequence 189139,
172	28	66.7	249	5	US-10-450-763-32317	Sequence 32317, A	245	28	66.7	751	4	US-10-437-963-189139	Sequence 189139,
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:04 ; Search time 7.89796 Seconds  
(without alignments)  
48.418 Million cell updates/sec

Title: US-10-067-484-2  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	78.6	605	US-11-087-099-3240	Sequence 3240, App
2	32	76.2	467	US-11-079-463-8954	Sequence 8954, App
3	32	76.2	713	US-11-052-554A-74	Sequence 74, App
4	31	73.8	1380	US-11-079-463-6036	Sequence 6036, App
5	30	71.4	426	US-10-467-657-2120	Sequence 2120, App
6	30	71.4	899	US-11-188-298-20608	Sequence 20608, App
7	29	69.0	107	US-11-004-590-234	Sequence 234, App
8	29	69.0	107	US-11-004-590-236	Sequence 236, App
9	29	69.0	107	US-11-004-590-275	Sequence 275, App
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17	29	69.0	107	US-11-004-590-283	Sequence 283, App
18	29	69.0	107	US-11-004-590-284	Sequence 284, App
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100	28	66.7	107	7	US-11-004-590-261	Sequence 261, App	173	27	64.3	575	7	US-11-096-568A-32502	Sequence 32502, A
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104	28	66.7	108	7	US-11-102-512-40	Sequence 40, App	177	27	64.3	620	7	US-11-113-424-70	Sequence 70, Appl
105	28	66.7	108	7	US-11-102-512-50	Sequence 50, Appl	178	27	64.3	631	7	US-11-087-099-10959	Sequence 10959, A
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136	28	66.7	923	7	US-11-007-428-6	Sequence 6, Appl1	209	26	61.9	263	7	US-11-087-099-834	Sequence 834, App
137	28	66.7	1075	7	US-11-089-551A-23	Sequence 23, Appl1	210	26	61.9	263	7	US-11-087-099-834	Sequence 834, App
138	28	66.7	160	7	US-11-079-463-7473	Sequence 7473, App	211	26	61.9	263	7	US-11-087-099-834	Sequence 834, App
139	27	64.3	219	7	US-11-096-568A-5521	Sequence 3521, App	212	26	61.9	275	7	US-11-096-568A-4253	Sequence 4253, App
140	27	64.3	223	7	US-11-079-463-675	Sequence 2, Appl1	213	26	61.9	281	7	US-11-096-568A-7759	Sequence 7759, App
141	27	64.3	223	7	US-11-079-463-675	Sequence 2, Appl1	214	26	61.9	296	7	US-11-096-568A-32174	Sequence 32174, A
142	27	64.3	223	7	US-11-079-463-675	Sequence 2, Appl1	215	26	61.9	301	7	US-11-096-568A-7758	Sequence 7758, App
143	27	64.3	223	7	US-11-079-463-675	Sequence 2, Appl1	216	26	61.9	307	7	US-11-188-298-360	Sequence 360, App
144	27	64.3	229	6	US-10-194-487-198	Sequence 198, App	217	26	61.9	307	7	US-11-188-298-360	Sequence 360, App
145	27	64.3	229	6	US-10-195-888-198	Sequence 198, App	218	26	61.9	307	7	US-11-188-298-360	Sequence 360, App
146	27	64.3	229	6	US-10-195-888-198	Sequence 198, App	219	26	61.9	309	7	US-11-096-568A-29339	Sequence 29339, A
147	27	64.3	229	6	US-10-195-888-198	Sequence 198, App	220	26	61.9	310	7	US-11-188-298-12746	Sequence 12746, A
148	27	64.3	229	6	US-10-195-888-198	Sequence 198, App	221	26	61.9	311	7	US-11-096-568A-4486	Sequence 4486, App
149	27	64.3	229	6	US-10-195-888-198	Sequence 198, App	222	26	61.9	312	7	US-11-096-568A-4485	Sequence 4485, App
150	27	64.3	289	7	US-11-079-463-8594	Sequence 8594, App	223	26	61.9	322	7	US-11-188-298-13208	Sequence 13208, A
151	27	64.3	303	7	US-11-079-463-8594	Sequence 8594, App	224	26	61.9	322	7	US-11-188-298-1364	Sequence 1364, App
152	27	64.3	347	7	US-11-096-568A-12503	Sequence 32503, A	225	26	61.9	324	7	US-11-096-568A-21907	Sequence 21907, A
153	27	64.3	376	7	US-11-096-568A-19934	Sequence 19934, A	226	26	61.9	324	7	US-11-188-298-824	Sequence 824, App
154	27	64.3	406	7	US-11-096-568A-19932	Sequence 19932, A	227	26	61.9	324	7	US-11-188-298-824	Sequence 824, App
155	27	64.3	406	7	US-11-096-568A-19932	Sequence 19932, A	228	26	61.9	324	7	US-11-188-298-824	Sequence 824, App
156	27	64.3	450	7	US-11-096-568A-11401	Sequence 31401, Appl	229	26	61.9	324	7	US-11-188-298-18250	Sequence 18250, A
157	27	64.3	450	7	US-11-096-568A-11401	Sequence 31401, Appl	230	26	61.9	324	7	US-11-188-298-18250	Sequence 18250, A
158	27	64.3	481	7	US-11-096-568A-31400	Sequence 31400, App	231	26	61.9	329	7	US-11-188-298-22315	Sequence 22315, A
159	27	64.3	481	7	US-11-096-568A-31400	Sequence 31400, App	232	26	61.9	331	7	US-11-188-298-12499	Sequence 12499, A
160	27	64.3	481	7	US-11-096-568A-31400	Sequence 31400, App	233	26	61.9	334	7	US-11-096-568A-32172	Sequence 32172, A
161	27	64.3	503	7	US-11-096-568A-31459	Sequence 31459, A	234	26	61.9	344	7	US-11-188-298-6045	Sequence 6045, App
162	27	64.3	519	7	US-11-087-099-6772	Sequence 7272, Appl	235	26	61.9	344	7	US-11-096-568A-2106	Sequence 2106, A
163	27	64.3	519	7	US-11-087-099-6772	Sequence 7272, Appl	236	26	61.9	344	7	US-11-096-568A-2106	Sequence 2106, A
164	27	64.3	519	7	US-11-087-099-6772	Sequence 7272, Appl	237	26	61.9	344	7	US-11-096-568A-2106	Sequence 2106, A
165	27	64.3	519	7	US-11-087-099-6772	Sequence 7272, Appl	238	26	61.9	344	7	US-11-096-568A-2106	Sequence 2106, A
166	27	64.3	519	7	US-11-087-099-6772	Sequence 7272, Appl	239	26	61.9	344	7	US-11-096-568A-2106	Sequence 2106, A
167	27	64.3	519	7	US-11-087-099-6772	Sequence 7272, Appl	240	26	61.9	344	7	US-11-096-568A-2106	Sequence 2106, A
168	27	64.3	519	7	US-11-087-099-6772	Sequence 7272, Appl	241	26	61.9	344	7	US-11-096-568A-2106	Sequence 2106, A
169	27	64.3	519	7	US-11-087-099-6772	Sequence 7272, Appl	242	26	61.9	344	7	US-11-096-568A-2106	Sequence 2106, A
170	27	64.3	519	7	US-11-087-099-6772	Sequence 7272, Appl	243	26	61.9	344	7	US-11-096-568A-2106	Sequence 2106, A
171	27	64.3	519	7	US-11-087-099-6772	Sequence 7272, Appl	244	26	61.9	344	7	US-11-096-568A-2106	Sequence 2106, A

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:40:47 ; Search time 90.7347 Seconds  
(without alignments)  
43.582 Million cell updates/sec

Title: US-10-067-484-3

Perfect score: 43

Sequence: 1 XYGLVQFNR 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

A\_Geneseq\_21:\*

1: geneseqp19808:\*

2: geneseqp19908:\*

3: geneseqp20008:\*

4: geneseqp20015:\*

5: geneseqp20025:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	9	5	ABB81970
2	33	76.7	99	4	AAU56543
3	33	76.7	99	6	ABM53062
4	33	76.7	170	6	ABU28434
5	33	76.7	192	7	ADM26790
6	33	76.7	253	5	ABP25912
7	33	76.7	253	8	ADV88395
8	33	76.7	253	8	ADV81810
9	33	76.7	253	8	ADV79648
10	33	76.7	329	3	AAU51794
11	33	76.7	383	9	AEA22843
12	33	76.7	819	9	ADA33363
13	33	76.7	16	6	ADY38298
14	33	76.7	112	4	ABB16566
15	33	76.7	124	2	AAV36180
16	33	76.7	124	2	AAV36133
17	33	76.7	124	2	AAV36210
18	33	76.7	124	2	AAV36210
19	33	76.7	124	2	AAV36210
20	33	76.7	124	2	AAV36210
21	33	76.7	124	2	AAV36210
22	33	76.7	124	2	AAV36210
23	33	76.7	124	2	AAV36210
24	33	76.7	124	2	AAV36210

25	32	74.4	124	8	ADP19441	Adp19441 Human sec
26	32	74.4	124	2	ADP19471	Adp19471 Human sec
27	32	74.4	132	2	AAV76521	AAV76521 Human ova
28	32	74.4	132	4	AAW41287	AAW41287 Human pol
29	32	74.4	291	5	ABG91467	ABG91467 Purine/pol
30	32	74.4	291	9	ABE38586	ABE38586 L. pneumo
31	32	74.4	291	9	ABE41828	ABE41828 L. pneumo
32	32	74.4	291	9	ADU30672	ADU30672 Bacterial
33	32	74.4	296	8	AAU15980	AAU15980 E. coli p
34	32	74.4	296	6	ABU14692	ABU14692 Protein e
35	32	74.4	323	2	AAU55360	AAU55360 H. pylori
36	32	74.4	323	2	AAU17165	AAU17165 H. pylori
37	32	74.4	476	2	AAW69946	AAW69946 GlucNAc1
38	32	74.4	751	9	ADU25498	ADU25498 Microbial
39	32	74.4	949	9	ADU25498	ADU25498 Hyperther
40	32	74.4	1282	8	ADU46345	ADU46345 Thermococ
41	31	72.1	57	8	ADU82034	ADU82034 Streptoco
42	31	72.1	57	8	ADU82034	ADU82034 Streptoco
43	31	72.1	58	8	ADU79888	ADU79888 Streptoco
44	31	72.1	203	4	AAU21601	AAU21601 Novel hum
45	31	72.1	203	7	ADU46242	ADU46242 Human neo
46	31	72.1	222	8	ADU44574	ADU44574 Bacterial
47	31	72.1	240	6	ABP80613	ABP80613 N. gonorr
48	31	72.1	343	4	ABE60195	ABE60195 Drosophila
49	31	72.1	380	7	ABW87681	ABW87681 Rice abio
50	31	72.1	394	4	ABP70391	ABP70391 Drosophila
51	31	72.1	460	5	ABP27238	ABP27238 Streptoco
52	31	72.1	460	8	ADU89577	ADU89577 Streptoco
53	31	72.1	460	8	ADU82984	ADU82984 Streptoco
54	31	72.1	460	8	ADU80830	ADU80830 Streptoco
55	31	72.1	514	7	ADP03970	ADP03970 Bacterial
56	31	72.1	514	7	ADP76282	ADP76282 Marker ge
57	31	72.1	752	8	ADU25075	ADU25075 Bacterial
58	31	72.1	791	6	ABR53460	ABR53460 Protein s
59	31	72.1	791	7	ADK64604	ADK64604 Disease t
60	31	72.1	796	5	ABP73364	ABP73364 Candida a
61	31	72.1	3580	7	ADN97367	ADN97367 E. lichen
62	30	69.8	62	4	AAW88001	AAW88001 Human imm
63	30	69.8	62	6	ABP75649	ABP75649 Human sec
64	30	69.8	134	7	ADU89489	ADU89489 Ribosomal
65	30	69.8	193	6	ABP78085	ABP78085 N. gonorr
66	30	69.8	265	8	ADU05599	ADU05599 M. catarr
67	30	69.8	294	8	ADP77666	ADP77666 Francisel
68	30	69.8	296	5	ABG91440	ABG91440 Purine/py
69	30	69.8	297	5	ABR49377	ABR49377 Listeria
70	30	69.8	297	5	ADY76842	ADY76842 Plant ful
71	30	69.8	304	2	AAW34599	AAW34599 Amaranthu
72	30	69.8	304	2	AAW85564	AAW85564 Seed stor
73	30	69.8	304	2	AAW83352	AAW83352 Amaranthu
74	30	69.8	304	5	AAO14934	AAO14934 Amaranthu
75	30	69.8	304	5	AAO14934	AAO14934 Amaranthu
76	30	69.8	304	5	AAO14934	AAO14934 Amaranthu
77	30	69.8	321	4	AAW70839	AAW70839 S. halste
78	30	69.8	328	3	AAW26632	AAW26632 Aribidops
79	30	69.8	357	7	ADU294618	ADU294618 E. faeciu
80	30	69.8	357	7	ABR55610	ABR55610 Lactococc
81	30	69.8	362	7	ADU85693	ADU85693 Enterococ
82	30	69.8	366	6	ADA36005	ADA36005 Acinetoba
83	30	69.8	373	6	ABU19966	ABU19966 Protein e
84	30	69.8	399	7	ADU94691	ADU94691 E. faeciu
85	30	69.8	399	7	ADU94691	ADU94691 Bacterial
86	30	69.8	402	5	ABP39293	ABP39293 Staphyloc
87	30	69.8	402	5	ADU505919	ADU505919 Staphyloc
88	30	69.8	448	8	ADY24894	ADY24894 Plant ful
89	30	69.8	501	4	ADU19802	ADU19802 Protein e
90	30	69.8	514	4	ADU87301	ADU87301 Novel cen
91	30	69.8	514	4	ADU20055	ADU20055 Protein e
92	30	69.8	514	8	ADU54616	ADU54616 Novel hum
93	30	69.8	547	8	ADU07361	ADU07361 Plant ful
94	30	69.8	553	8	ADU96602	ADU96602 Plant ful
95	30	69.8	584	6	ABU49543	ABU49543 Protein e
96	30	69.8	605	8	ADY13197	ADY13197 Plant ful
97	30	69.8	625	6	ABP72781	ABP72781 Avocado 9

98	30	69.8	652	9	ADY60941	Abiolic B	171	29	67.4	292	5	ABG91423	Abg91423	Purine/py
99	30	69.8	712	8	ADN47191	Adn47190 Thermococ	172	29	67.4	293	5	ABG91428	Abg91428	Purine/py
100	30	69.8	712	8	ABU29538	Abu29538 Protein e	173	29	67.4	293	5	ABG91429	Abg91429	Purine/py
101	30	69.8	718	2	ABW13384	Abw13384 Human pro	174	29	67.4	293	8	ADN18234	Adn18234 Bacterial	
102	30	69.8	748	4	ABJ31477	Abj31477 Humno aci	175	29	67.4	293	8	ABW83480	Abw83480 Human dia	
103	30	69.8	748	4	ADN95750	Adn95750 Human BRC	176	29	67.4	296	2	AAR55350	Aar55350 Wheat sec	
104	30	69.8	748	4	ADN95750	Adn95750 Human BRC	177	29	67.4	303	5	ADG79547	Adg79547 Human sec	
105	30	69.8	748	4	ADN95750	Adn95750 Human BRC	178	29	67.4	304	3	AAG25236	Aag25236 Arabidops	
106	30	69.8	748	4	ADN95750	Adn95750 Human BRC	179	29	67.4	306	8	ADY11224	Ady11224 Plant ful	
107	30	69.8	752	8	ADN25708	Adn25708 PRO polYP	180	29	67.4	316	4	ABW62195	Abw62195 Drosophi	
108	30	69.8	752	8	ADN25708	Adn25708 Bacteri	181	29	67.4	325	8	ADN19887	Adn19887 Bacterial	
109	30	69.8	752	8	ADN25708	Adn25708 Bacteri	182	29	67.4	377	8	ADN47167	Adn47167 Thermococ	
110	30	69.8	752	8	ADN25708	Adn25708 Bacteri	183	29	67.4	377	8	ADN47167	Adn47167 Thermococ	
111	30	69.8	804	4	ADN95444	Adn95444 E. faeciu	184	29	67.4	390	5	ABW59221	Abw59221 Drosophi	
112	30	69.8	831	8	ADN05464	Adn05464 Antipepti	185	29	67.4	390	5	ABW59221	Abw59221 Drosophi	
113	30	69.8	932	6	ABW97913	Abw97913 Protein e	186	29	67.4	390	5	ABW59221	Abw59221 Drosophi	
114	30	69.8	960	6	ABW97913	Abw97913 Antino aci	187	29	67.4	395	4	ABW29664	Abw29664 Protein e	
115	30	69.8	1035	4	ABW61120	Abw61120 Drosophi	188	29	67.4	414	8	ADY23962	Ady23962 Plant ful	
116	30	69.8	1038	6	ABW25711	Abw25711 Protein e	189	29	67.4	419	3	ABW53327	Abw53327 Arabidops	
117	30	69.8	1179	6	ABW47667	Abw47667 Listeria	190	29	67.4	437	4	ABW17017	Abw17017 Novel hum	
118	30	69.8	1179	6	ABW47667	Abw47667 Listeria	191	29	67.4	440	6	ABW63425	Abw63425 Drosophi	
119	30	69.8	1874	4	ABW76532	Abw76532 Corymbac	192	29	67.4	456	6	ABW53249	Abw53249 Protein s	
120	30	69.8	2071	5	ABW74125	Abw74125 Mouse mas	193	29	67.4	476	7	ADK63662	Adk63662 Disease t	
121	30	69.8	2701	5	ABW74125	Abw74125 Mouse TRI	194	29	67.4	482	7	ADK63662	Adk63662 Disease t	
122	30	69.8	2747	8	ADN62964	Adn62964 Human NOV	195	29	67.4	487	6	ABW49180	Abw49180 Protein e	
123	30	69.8	2753	6	ADN62964	Adn62964 Human NOV	196	29	67.4	487	6	ABW49180	Abw49180 Protein e	
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125	30	69.8	2753	6	ADN62964	Adn62964 Human NOV	198	29	67.4	487	6	ABW49180	Abw49180 Protein e	
126	30	69.8	2777	8	AAE10925	Aae10925 Human mon	199	29	67.4	487	6	ABW49180	Abw49180 Protein e	
127	30	69.8	2777	8	AAE10925	Aae10925 Human mon	200	29	67.4	487	6	ABW49180	Abw49180 Protein e	
128	30	69.8	2780	4	AAE10924	Aae10924 Mouse mon	201	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
129	30	69.8	2780	4	AAE10924	Aae10924 Mouse mon	202	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
130	30	69.8	2969	7	ADL65607	Adl65607 C. glutam	203	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
131	30	69.8	3040	8	ADN88306	Adn88306 Brevibact	204	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
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158	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	231	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
159	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	232	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
160	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	233	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
161	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	234	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
162	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	235	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
163	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	236	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
164	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	237	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
165	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	238	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
166	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	239	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
167	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	240	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
168	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	241	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
169	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	242	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	
170	30	69.8	3062	8	ADN88306	Adn88306 Brevibact	243	29	67.4	500	2	ABW53351	Abw53351 Wheat lea	

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:12 ; Search time 8.26511 Seconds  
(without alignments)  
104.769 Million cell updates/sec

Title: US-10-067-484-3  
Perfect score: 43  
Sequence: 1 XYGIVQFNR 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :  
1: PIR 80:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	76.7	63	2 D69115	hypothetical prote
2	33	76.7	650	2 T32897	hypothetical prote
3	33	76.7	662	2 T47649	ABC transporter-1i
4	32	74.4	296	2 H90896	hypothetical prote
5	32	74.4	296	2 G85720	hypothetical prote
6	32	74.4	296	2 B64908	yeast protein - Bsc
7	32	74.4	417	2 C69795	glutanyl-tRNA (Gln)
8	32	74.4	476	2 T51583	glutanyl-tRNA (Gln)
9	32	74.4	476	2 T44293	glutanyl-tRNA (Gln)
10	32	74.4	751	2 D71860	probable outer mem
11	31	72.1	152	2 B64842	probable monooxyge
12	31	72.1	152	2 B90785	probable 4-hydroxy
13	31	72.1	152	2 C85645	probable 4-hydroxy
14	31	72.1	345	2 S72490	N-acetyl-gamma-glu
15	31	72.1	364	2 A70474	conserved hypotet
16	31	72.1	428	2 T03934	DNA binding protei
17	31	72.1	482	2 T01932	RNA binding protei
18	31	72.1	570	2 C66440	hypothetical prote
19	31	72.1	791	2 S61698	hypothetical prote
20	31	72.1	794	1 S37606	SRG18 protein - ye
21	31	72.1	3655	2 T38084	TRAP-like protein
22	30	69.8	47	2 F81235	hypothetical prote
23	30	69.8	81	2 T06548	retrovirus-related
24	30	69.8	88	2 B47760	ribosomal protein
25	30	69.8	123	2 T43380	hypothetical prote
26	30	69.8	133	2 G91092	60s ribosomal prot
27	30	69.8	136	2 T37749	hypothetical prote
28	30	69.8	136	2 T19479	hypothetical prote
29	30	69.8	167	2 C85938	hypothetical prote

30	30	69.8	207	2 T03331	gene e3f protein -
31	30	69.8	223	2 H87335	conserved hypotet
32	30	69.8	229	2 A81169	hypothetical prote
33	30	69.8	231	2 G81936	hypothetical prote
34	30	69.8	292	2 A97512	glucose 1-dehydrog
35	30	69.8	296	2 D75597	glucose-1-phosphat
36	30	69.8	297	2 AC1706	hypothetical prote
37	30	69.8	297	2 AD1335	hypothetical prote
38	30	69.8	304	2 S24263	seed storage prote
39	30	69.8	357	2 G86906	hypothetical prote
40	30	69.8	400	2 G83790	aminotransferase B
41	30	69.8	404	2 F71718	alanine racemase (
42	30	69.8	408	2 C70379	hypothetical prote
43	30	69.8	449	2 T48511	aspartate transami
44	30	69.8	468	2 T33516	hypothetical prote
45	30	69.8	474	2 AB2161	hypothetical prote
46	30	69.8	514	2 B84290	hypothetical prote
47	30	69.8	548	2 T41182	probable protein p
48	30	69.8	555	2 A45697	immediate-early pr
49	30	69.8	584	2 G82079	single-stranded-DN
50	30	69.8	638	2 S37085	polyadenylate-bind
51	30	69.8	651	2 T06979	polyadenylate-bind
52	30	69.8	655	2 T00768	polyadenylate-bind
53	30	69.8	668	2 B96740	hypothetical prote
54	30	69.8	720	2 A13420	hypothetical prote
55	30	69.8	718	2 T47648	ABC transporter-1i
56	30	69.8	757	2 AC2691	penicillin binding
57	30	69.8	757	2 G97472	penicillin-binding
58	30	69.8	867	1 RRVCCV	RNA-directed RNA p
59	30	69.8	967	2 T15680	hypothetical prote
60	30	69.8	1179	2 AG1101	transcription-repa
61	30	69.8	1179	2 AG1463	transcription-repa
62	30	69.8	1179	2 S55505	fatty-acid synchas
63	30	69.8	285	2 AG2963	conserved hypotet
64	29.5	68.6	320	2 F98319	hypothetical prote
65	29	67.4	93	2 A72653	hypothetical prote
66	29	67.4	149	2 S22209	photosystem I chla
67	29	67.4	168	2 H89886	hypothetical prote
68	29	67.4	220	1 VYBPFE	phage lysis protei
69	29	67.4	227	2 C58932	channel subunit of
70	29	67.4	229	2 A37775	phob protein - Pse
71	29	67.4	229	2 AG0698	probable pathogeni
72	29	67.4	232	2 T44456	arginine/ornithine
73	29	67.4	277	2 H70159	ribosomal protein
74	29	67.4	288	2 AE1313	hypothetical prote
75	29	67.4	288	2 AE1585	hypothetical prote
76	29	67.4	289	2 A87391	glucose-1-phosphat
77	29	67.4	290	1 S06477	glucose-1-phosphat
78	29	67.4	293	1 F64969	glucose-1-phosphat
79	29	67.4	294	2 C72378	sugar ABC transpor
80	29	67.4	296	2 S05078	glucose-1-phosphat
81	29	67.4	333	2 D97356	uncharacterized pr
82	29	67.4	343	2 S77079	hypothetical prote
83	29	67.4	363	2 D96900	recf, ABC family A
84	29	67.4	384	2 S64074	hypothetical prote
85	29	67.4	402	2 T25363	hypothetical prote
86	29	67.4	410	2 T15442	hypothetical prote
87	29	67.4	442	2 H69181	NADH2 dehydrogenas
88	29	67.4	462	2 T11136	PEP12 homolog - M
89	29	67.4	472	2 A64320	probable Glu-tRNA
90	29	67.4	476	2 A56510	D-alanyl-D-alanine
91	29	67.4	486	2 B72554	glutanyl-tRNA (Gln)
92	29	67.4	487	2 H82298	glutanyl-tRNA (Gln)
93	29	67.4	491	2 A11980	glucose-1-phosphat
94	29	67.4	500	2 S05077	hypothetical prote
95	29	67.4	502	2 G70193	glucose-1-phosphat
96	29	67.4	514	2 T04155	glucose-1-phosphat
97	29	67.4	518	2 T02965	glucose-1-phosphat
98	29	67.4	519	2 T02965	glucose-1-phosphat
99	29	67.4	521	2 S49439	glucose-1-phosphat
100	29	67.4	522	2 S60572	glucose-1-phosphat
101	29	67.4	527	2 S24984	glucose-1-phosphat
102	29	67.4	559	2 B95120	site-specific reco

gene e3f protein -  
conserved hypotet  
hypothetical prote  
hypothetical prote  
glucose 1-dehydrog  
glucose-1-phosphat  
hypothetical prote  
hypothetical prote  
seed storage prote  
hypothetical prote  
aminotransferase B  
alanine racemase (  
hypothetical prote  
aspartate transami  
hypothetical prote  
hypothetical prote  
probable protein p  
immediate-early pr  
single-stranded-DN  
polyadenylate-bind  
polyadenylate-bind  
polyadenylate-bind  
hypothetical prote  
hypothetical prote  
ABC transporter-1i  
penicillin binding  
penicillin-binding  
RNA-directed RNA p  
hypothetical prote  
transcription-repa  
transcription-repa  
fatty-acid synchas  
conserved hypotet  
hypothetical prote  
hypothetical prote  
photosystem I chla  
hypothetical prote  
phage lysis protei  
channel subunit of  
phob protein - Pse  
probable pathogeni  
arginine/ornithine  
ribosomal protein  
hypothetical prote  
glucose-1-phosphat  
glucose-1-phosphat  
glucose-1-phosphat  
sugar ABC transpor  
glucose-1-phosphat  
uncharacterized pr  
hypothetical prote  
recf, ABC family A  
hypothetical prote  
hypothetical prote  
hypothetical prote  
NADH2 dehydrogenas  
PEP12 homolog - M  
probable Glu-tRNA  
D-alanyl-D-alanine  
glutanyl-tRNA (Gln)  
glucose-1-phosphat  
hypothetical prote  
glucose-1-phosphat  
glucose-1-phosphat  
glucose-1-phosphat  
glucose-1-phosphat  
glucose-1-phosphat  
site-specific reco

103	29	67.4	559	2	F97989	site-specific reco
104	29	67.4	562	2	A96713	hypothetical prote
105	29	67.4	570	2	G68038	protein P18A12.3 l
106	29	67.4	581	2	B6852	sugar transport sy
107	29	67.4	609	2	T00497	probable poly(A) b
108	29	67.4	682	2	G9447	polyadenylate-bind
109	29	67.4	734	2	T34508	hypothetical prote
110	29	67.4	740	1	T02567	culin-4 - fission
111	29	67.4	1047	2	T34946	probable ATP-bind
112	29	67.4	1146	2	A11208	pyruvate isoenzym
113	29	67.4	1146	2	AC1565	pyruvate carboxyla
114	29	67.4	1388	2	E82533	RNA polymerase Dc
115	29	66.3	497	2	S47890	exuperantial 1
116	28	65.1	69	2	D90905	hypothetical prote
117	28	65.1	89	2	F90386	transcription regu
118	28	65.1	98	2	T42909	hypothetical prote
119	28	65.1	116	2	D91755	hypothetical prote
120	28	65.1	183	2	A12274	hypothetical prote
121	28	65.1	185	2	AF2236	hypothetical prote
122	28	65.1	187	2	T15478	hypothetical prote
123	28	65.1	206	2	G69387	hypothetical prote
124	28	65.1	230	2	H60387	probable permease
125	28	65.1	231	2	G69271	decapping enzyme C
126	28	65.1	252	2	H60476	molybdopterin oxid
127	28	65.1	285	2	S63260	hypothetical prote
128	28	65.1	288	2	H80476	hypothetical prote
129	28	65.1	288	2	H82014	glucose-1-phosphat
130	28	65.1	290	2	F83859	hypothetical prote
131	28	65.1	291	2	AB1487	hypothetical prote
132	28	65.1	292	2	AD0767	glucose-1-phosphat
133	28	65.1	292	2	S23342	glucose-1-phosphat
134	28	65.1	293	2	S15301	glucose-1-phosphat
135	28	65.1	293	2	D83000	homoserine O-succ
136	28	65.1	309	1	XYECM	homoserine transu
137	28	65.1	309	2	AC1011	homoserine transu
138	28	65.1	309	2	A86093	calpain (EC 3.4.22
139	28	65.1	309	2	G91845	probable glucosyl
140	28	65.1	320	2	G24493	hypothetical prote
141	28	65.1	320	2	AD0979	hypothetical prote
142	28	65.1	320	2	G90492	hypothetical prote
143	28	65.1	332	2	A65157	hypothetical prote
144	28	65.1	332	2	G90492	hypothetical prote
145	28	65.1	332	2	A65157	hypothetical prote
146	28	65.1	332	2	A65157	hypothetical prote
147	28	65.1	332	2	A65157	hypothetical prote
148	28	65.1	332	2	A65157	hypothetical prote
149	28	65.1	332	2	A65157	hypothetical prote
150	28	65.1	332	2	A65157	hypothetical prote
151	28	65.1	332	2	A65157	hypothetical prote
152	28	65.1	332	2	A65157	hypothetical prote
153	28	65.1	332	2	A65157	hypothetical prote
154	28	65.1	332	2	A65157	hypothetical prote
155	28	65.1	332	2	A65157	hypothetical prote
156	28	65.1	332	2	A65157	hypothetical prote
157	28	65.1	332	2	A65157	hypothetical prote
158	28	65.1	332	2	A65157	hypothetical prote
159	28	65.1	332	2	A65157	hypothetical prote
160	28	65.1	332	2	A65157	hypothetical prote
161	28	65.1	332	2	A65157	hypothetical prote
162	28	65.1	332	2	A65157	hypothetical prote
163	28	65.1	332	2	A65157	hypothetical prote
164	28	65.1	332	2	A65157	hypothetical prote
165	28	65.1	332	2	A65157	hypothetical prote
166	28	65.1	332	2	A65157	hypothetical prote
167	28	65.1	332	2	A65157	hypothetical prote
168	28	65.1	332	2	A65157	hypothetical prote
169	28	65.1	332	2	A65157	hypothetical prote
170	28	65.1	332	2	A65157	hypothetical prote
171	28	65.1	332	2	A65157	hypothetical prote
172	28	65.1	332	2	A65157	hypothetical prote
173	28	65.1	332	2	A65157	hypothetical prote
174	28	65.1	332	2	A65157	hypothetical prote
175	28	65.1	332	2	A65157	hypothetical prote

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:05 ; Search time 49.0408 Seconds  
(without alignments)  
129.479 Million cell updates/sec

Title: US-10-067-484-3  
Perfect score: 43  
Sequence: 1 XYGLVQFNR 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_tramb1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	88.4	443	04MDR7 ASPFU	Q4wdt7 aepexgillus
2	38	88.4	678	05LIH0_BACRY	Q5liho bacteroides
3	38	88.4	678	064ZU4_BACFR	Q64z44 bacteroides
4	34	79.1	242	054P36_DICDI	Q54p36 dictyosteli
5	34	79.1	304	083AP7_COXBU	Q83ap7 coxiella bu
6	34	79.1	354	1 ARGC_BORBR	Q7wfc5 bordetella
7	34	79.1	354	1 ARGC_BORPA	Q7w3z3 bordetella
8	34	79.1	354	1 ARGC_BORPE	Q7wuo0 bordetella
9	33	76.7	63	027885_METTH	Q27885 methanobact
10	33	76.7	124	06Y228_PAGMA	Q6y228 pagrus majo
11	33	76.7	124	050386_BRARE	Q50386 brachydanio
12	33	76.7	124	04SSFS_TETNG	Q4ssfs tetradodon n
13	33	76.7	192	08TVJ3_METKA	Q8tvj3 methanopyru
14	33	76.7	253	1 RECO_STRAS	Q8e7x6 streptococc
15	33	76.7	253	1 RECO_STRAS	Q8e298 streptococc
16	33	76.7	275	061104_CAEBR	Q61104 caenorhabdi
17	33	76.7	278	057UW9_GTRYP	Q57uw9 trypanosoma
18	33	76.7	313	044967_CAEEL	Q44967 caenorhabdi
19	33	76.7	333	08SRU7_NACEU	Q8sr77 encephalito
20	33	76.7	463	050U64_ENTHI	Q50u64 entamoeba h
21	33	76.7	533	08DHX4_SYNEL	Q8dhx4 synechococc
22	33	76.7	618	1 XYLA2_BACST	Q49674 bacillus st
23	33	76.7	662	061S93_CAEBR	Q61s93 caenorhabdi
24	33	76.7	662	09M2V6_ARATH	Q9m2v6 arabidopsis
25	33	76.7	1439	05TVAI_ANOGA	Q5tvai anopheles g
26	32	74.4	124	1 MKI11_HUMAN	Q8gha4 homo sapien
27	32	74.4	124	1 MKI11_MOUSE	Q88653 mus musculu
28	32	74.4	124	053FR6_HUMAN	Q53fr6 homo sapien
29	32	74.4	124	05R3Z6_PONPY	Q5r3z6 ponpy
30	32	74.4	124	054217_MOUSE	Q54217 mus musculu
31	32	74.4	124	05U204_RAT	Q5u204 rattus norv

32	32	74.4	124	2 05Z1P2_CHICK	Q5z1p2 gallus gall
33	32	74.4	148	2 05K592_ORYSA	Q5k592 oryza sativ
34	32	74.4	166	2 05HMM0_STABO	Q5hmm0 staphylococ
35	32	74.4	260	2 05KUB0_GEOKA	Q5kub0 geobacillus
36	32	74.4	262	2 06A070_MERCA	Q6a070 methylococc
37	32	74.4	291	2 09RDY3_LEGEN	Q9rdy3 legionella
38	32	74.4	291	2 04USZ4_CORX	Q4usz4 corynebacte
39	32	74.4	291	2 05WYD9_LEGPH	Q5wyd9 legionella
40	32	74.4	291	2 05XEV7_LEGPA	Q5xev7 legionella
41	32	74.4	293	2 082WJ7_NITPU	Q82wj7 nitrosomona
42	32	74.4	296	1 YDEH_ECOLI	P31129 escherichia
43	32	74.4	296	2 08XB26_ECO57	Q8xb26 escherichia
44	32	74.4	298	2 08FHD4_ECOL6	Q8fhd4 escherichia
45	32	74.4	299	2 07MGN4_WOLES	Q7mgn4 wolfinella s
46	32	74.4	305	2 05ZXH1_LEGPH	Q5zxh1 legionella
47	32	74.4	321	2 06ASCI_DESPS	Q6asci desulfatole
48	32	74.4	359	2 05LO45_SILPO	Q5lq45 silicibacte
49	32	74.4	395	2 05ZRY3_LEGPH	Q5zry3 legionella
50	32	74.4	426	2 07PUT5_ANOGA	Q7put5 anopheles g
51	32	74.4	439	2 09LIY4_ORYSA	Q9liy4 oryza sativ
52	32	74.4	444	2 06Z9W0_ORYSA	Q6z9w0 oryza sativ
53	32	74.4	444	2 082B32_STRAM	Q82b32 streptomyce
54	32	74.4	445	2 09PBU4_ASPEU	Q9pbu4 aspergillus
55	32	74.4	475	2 04WM30_ASPEU	Q4wm30 aspergillus
56	32	74.4	476	1 GATB_BACST	Q929x0 bacillus ha
57	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
58	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
59	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
60	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
61	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
62	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
63	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
64	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
65	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
66	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
67	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
68	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
69	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
70	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
71	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
72	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
73	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
74	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
75	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
76	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
77	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
78	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
79	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
80	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
81	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
82	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
83	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
84	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
85	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
86	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
87	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
88	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
89	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
90	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
91	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
92	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
93	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
94	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
95	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
96	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
97	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
98	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
99	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
100	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
101	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
102	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
103	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su
104	32	74.4	476	1 GATB_BACST	Q931e1 bacillus su



105	31	72.1	394	2	Q9V36_DROME	Q9V36_drosophila	178	30	69.8	229	2	Q9K06_NEIMB	Q9K06_neisseria m
106	31	72.1	399	2	Q67R4_VIRU	Q67R4_lymphocystis	179	30	69.8	230	2	Q8178_CAEEL	Q8178_caenorhabdi
107	31	72.1	408	2	Q7WH9_HABPU	Q7WH9_haemophilus	180	30	69.8	231	2	Q9JVC1_NEIMA	Q9JVC1_neisseria m
108	31	72.1	412	2	Q4WAL4_ASPPU	Q4WAL4_aspergillus	181	30	69.8	232	2	Q6B39_CARMV	Q6B39_carnation m
109	31	72.1	421	2	Q7X289_SPLAN	Q7X289_gemmatia sp.	182	30	69.8	245	2	Q9DJVS_CARMV	Q9DJVS_carnation m
110	31	72.1	428	2	P33843_TOBAC	P33843_nicotiana t	183	30	69.8	245	2	Q9G6X8_CARMV	Q9G6X8_carnation m
111	31	72.1	429	2	Q9LEB3_NICPL	Q9LEB3_nicotiana p	184	30	69.8	249	2	Q6SE99_CAUD	Q6SE99_lactobacilli
112	31	72.1	432	2	Q9USPO_LAMPL	Q9USPO_lamproloma f1	185	30	69.8	249	2	Q6SPW0_LACIO	Q6SPW0_lactobacilli
113	31	72.1	433	2	Q5BMO6_SCHOL	Q5BMO6_schistosoma	186	30	69.8	273	2	Q6ZJ00_ORYSA	Q6ZJ00_oryza sativ
114	31	72.1	432	2	Q5BMO6_SCHOL	Q5BMO6_schistosoma	187	30	69.8	274	2	Q5LEW7_LEPIN	Q5LEW7_leptocystis
115	31	72.1	436	2	Q7YMS_9CAUD	Q7YMS_bacteriophila	188	30	69.8	280	2	Q5LEW7_LEPIN	Q5LEW7_leptocystis
116	31	72.1	444	2	Q5AKY3_CANAL	Q5AKY3_candida alb	189	30	69.8	282	2	Q4GZU4_LYCPM	Q4GZU4_lycopersico
117	31	72.1	460	2	Q8DY16_STRAS	Q8DY16_streptococc	190	30	69.8	282	2	Q4GZU3_LYCPM	Q4GZU3_lycopersico
118	31	72.1	460	2	Q8DY16_STRAS	Q8DY16_streptococc	191	30	69.8	282	2	Q4GZU2_LYCPM	Q4GZU2_lycopersico
119	31	72.1	478	2	Q8HKA7_9GAST	Q8HKA7_tobaccostrae	192	30	69.8	282	2	Q4GZU1_LYCPM	Q4GZU1_lycopersico
120	31	72.1	482	2	Q48955_TOBAC	Q48955_nicotiana t	193	30	69.8	292	2	Q4GZT9_LYCPM	Q4GZT9_lycopersico
121	31	72.1	508	2	Q72FM2_DESVH	Q72FM2_desulfovibrio	194	30	69.8	292	2	Q7CZNO_AGRTS	Q7CZNO_agrobacteri
122	31	72.1	515	2	Q4MA88_ASPPU	Q4MA88_aspergillus	195	30	69.8	294	2	Q79RC5_FRATT	Q79RC5_fractura
123	31	72.1	521	2	Q9MD18_SCEOB	Q9MD18_scenedesmus	196	30	69.8	296	2	Q9RZB2_DEIRA	Q9RZB2_detrinococcus
124	31	72.1	529	2	Q4K961_PSEFS	Q4K961_pseudomonas	197	30	69.8	297	2	Q8YSH8_LISMO	Q8YSH8_listeria mo
125	31	72.1	534	1	FM03_MOUSE	P97501_mus musculus	198	30	69.8	300	2	Q74BF8_GEOSL	Q74BF8_geobacter s
126	31	72.1	549	2	Q4WKJ3_ASPPU	Q4WKJ3_aspergillus	199	30	69.8	300	2	Q8S390_AMAHP	Q8S390_amaranthus
127	31	72.1	557	2	Q4UJZ7_RICFE	Q4UJZ7_rickettsia	200	30	69.8	304	2	Q7IOF2_AMACA	Q7IOF2_amaranthus
128	31	72.1	570	2	Q9C866_ARATH	Q9C866_arabidopsis	201	30	69.8	304	2	Q6YKX3_AMACA	Q6YKX3_amaranthus
129	31	72.1	577	2	Q5AZP2_EMENT	Q5AZP2_aspergillus	202	30	69.8	304	2	Q87L19_CAEEL	Q87L19_caenorhabdi
130	31	72.1	590	2	Q81L05_PLAF7	Q81L05_plasmodium	203	30	69.8	313	2	Q817L9_CAEEL	Q817L9_caenorhabdi
131	31	72.1	599	2	Q7R2B0_GIALA	Q7R2B0_giardia lam	204	30	69.8	320	2	Q6AGS6_LEITX	Q6AGS6_leifsonia x
132	31	72.1	629	2	Q6KQI5_DESPS	Q6KQI5_desulfohalate	205	30	69.8	321	2	Q84684_VYIRU	Q84684_peanut chlo
133	31	72.1	635	2	Q9C7B0_ARATH	Q9C7B0_arabidopsis	206	30	69.8	321	2	Q5WJH2_BACSK	Q5WJH2_streptomyc
134	31	72.1	638	2	Q9LH81_ARATH	Q9LH81_arabidopsis	207	30	69.8	354	2	Q9CDG5_LACIO	Q9CDG5_lactococcus
135	31	72.1	701	2	Q6PEH8_BRARE	Q6PEH8_brachydanio	208	30	69.8	357	2	Q6DLA4_CIOIN	Q6DLA4_ciona intes
136	31	72.1	720	2	Q54105_DICDI	Q54105_dicystosella	209	30	69.8	361	2	Q51965_BACIO	Q51965_bacteroides
137	31	72.1	741	2	Q8H0H2_TOBAC	Q8H0H2_nicotiana t	210	30	69.8	362	2	Q6MMB1_BDEBA	Q6MMB1_bdellovibrio
138	31	72.1	753	2	Q5CT65_CRYPV	Q5CT65_cryptospori	211	30	69.8	366	2	Q9T7C2_CAEEL	Q9T7C2_caenorhabdi
139	31	72.1	757	2	Q6N8N6_RHOPA	Q6N8N6_rhodospirillum	212	30	69.8	367	2	Q61CMB_CAEEL	Q61CMB_caenorhabdi
140	31	72.1	777	2	Q8CANG_MOUSE	Q8CANG_mus musculus	213	30	69.8	368	2	Q861M6_MYXGL	Q861M6_myxine glut
141	31	72.1	791	1	ELC18_YEAST	Q12050_saccharomyce	214	30	69.8	373	2	Q41NM6_9BURK	Q41NM6_burkholderi
142	31	72.1	794	1	SECT18_CRYPV	P34732_candida alb	215	30	69.8	373	2	Q4ZPP7_PSSSM	Q4ZPP7_pseudomonas
143	31	72.1	805	2	Q5CTU6_CRYPV	Q5CTU6_cryptospori	216	30	69.8	374	2	Q6ZERR6_BURMA	Q6ZERR6_burkholderi
144	31	72.1	805	2	Q5CH66_CRYHO	Q5CH66_cryptospori	217	30	69.8	377	2	Q63Y99_BURPS	Q63Y99_burkholderi
145	31	72.1	808	2	Q94A27_ARATH	Q94A27_arabidopsis	218	30	69.8	377	2	Q4WJ53_ASPPU	Q4WJ53_burkholderi
146	31	72.1	816	2	Q9LJG4_ARATH	Q9LJG4_arabidopsis	219	30	69.8	383	2	Q7VX55_BORBP	Q7VX55_bordelella
147	31	72.1	861	2	ENTX_MOUSE	P97435_mus musculus	220	30	69.8	383	2	Q7W821_BORBP	Q7W821_bordelella
148	31	72.1	1069	1	Q72A44_DESVH	Q72A44_desulfovibrio	221	30	69.8	383	2	Q7VX55_BORBP	Q7VX55_bordelella
149	31	72.1	1657	2	Q726X2_MIMIV	Q726X2_mimivirius	222	30	69.8	383	2	Q7W821_BORBP	Q7W821_bordelella
150	31	72.1	2221	2	Q81259_PLAF7	Q81259_plasmodium	223	30	69.8	383	2	Q7W821_BORBP	Q7W821_bordelella
151	31	72.1	2221	2	Q6SNNK5_BACLD	Q6SNNK5_bacillus 11	224	30	69.8	400	2	Q9KDP4_BACDD	Q9KDP4_bacillus ha
152	31	72.1	3580	2	Q6SNNK5_BACLD	Q6SNNK5_bacillus 11	225	30	69.8	400	2	Q9KDP4_BACDD	Q9KDP4_bacillus ha
153	31	72.1	3583	2	Q45295_BACLI	Q45295_bacillus 11	226	30	69.8	402	2	Q8CNP9_STABO	Q8CNP9_staphylococ
154	31	72.1	3655	1	YAMB_SCHPO	Q10064_schistosoma	227	30	69.8	402	2	Q8CNP9_STABO	Q8CNP9_staphylococ
155	31	72.1	47	2	Q9KJ12_NEIMB	Q9KJ12_neisseria m	228	30	69.8	408	1	YALT_RICR	YALT_rickettsia
156	31	69.8	57	2	Q7R6E1_GIALA	Q7R6E1_giardia lam	229	30	69.8	408	1	YALT_RICR	YALT_rickettsia
157	31	69.8	70	2	Q5KX15_GEOXA	Q5KX15_geobacillus	230	30	69.8	415	2	Q61M63_CAEEL	Q61M63_caenorhabdi
158	31	69.8	81	2	Q9ZRL6_WHEAT	Q9ZRL6_wheat	231	30	69.8	415	2	Q5Z862_ORYSA	Q5Z862_oryza sativ
159	31	69.8	88	2	Q6S300_WHEAT	Q6S300_wheat	232	30	69.8	417	2	Q5ZY04_NOCRA	Q5ZY04_nocardia fa
160	31	69.8	92	2	P93686_SECCCE	P93686_sectaria cere	233	30	69.8	417	2	Q9R667_LYCES	Q9R667_lycopersico
161	31	69.8	109	2	Q8H587_ORYSA	Q8H587_oryza sativ	234	30	69.8	428	2	Q8BHX2_SHEON	Q8BHX2_sheanella
162	31	69.8	119	2	Q6BUP1_DBHNA	Q6BUP1_debaryomyce	235	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
163	31	69.8	122	2	Q6NDAP_RHOPA	Q6NDAP_rhodospirillum	236	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
164	31	69.8	134	1	YFPE_SCHPO	Q14069_schistosoma	237	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
165	31	69.8	136	2	Q18208_CAEEL	Q18208_caenorhabdi	238	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
166	31	69.8	152	1	P8AL_GUTTH	Q78469_guillardiella	239	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
167	31	69.8	167	1	P8AL_ECO57	Q8X6H3_eschscholzia	240	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
168	31	69.8	172	2	Q4P7R8_USGMA	Q4P7R8_ustilago ma	241	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
169	31	69.8	181	2	Q5Y2F4_9HIV1	Q5Y2F4_human immun	242	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
170	31	69.8	183	2	Q8XYS3_RALSO	Q8XYS3_ralstonia s	243	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
171	31	69.8	191	2	Q8D7F7_VIBUV	Q8D7F7_vibrio vuln	244	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
172	31	69.8	192	2	Q9N3H6_CAEEL	Q9N3H6_caenorhabdi	245	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
173	31	69.8	195	2	Q7MEG7_VIBUV	Q7MEG7_vibrio vuln	246	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
174	31	69.8	207	2	Q80124_9CAUD	Q80124_bacteriophila	247	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
175	31	69.8	210	2	Q7ZNB5_9HIV1	Q7ZNB5_human immun	248	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
176	31	69.8	215	2	Q5DNB5_9HIV1	Q5DNB5_leptocystis	249	30	69.8	443	2	Q8RGR9_BRARE	Q8RGR9_burkholderi
177	31	69.8	223	2	Q9AAA7_CAUCR	Q9AAA7_caulobacter	250	30	69.8	443	2	Q5L1C4_GEOXA	Q5L1C4_geobacillus

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:21 ; Search time 17.449 Seconds  
(without alignments)  
42.643 Million cell updates/sec

Title: US-10-067-484-3  
Perfect score: 43  
Sequence: 1 XYGIVQFNR 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5 COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/6 COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/H COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/RB COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	76.7	819	2	US-09-328-352-4650	Sequence 4650, Ap
2	32	74.4	124	2	US-09-663-600A-91	Sequence 91, Appl
3	32	74.4	124	2	US-09-663-600A-185	Sequence 185, App
4	32	74.4	124	2	US-09-663-600A-215	Sequence 215, App
5	32	74.4	124	2	US-09-621-976-14	Sequence 14, Appl
6	32	74.4	296	2	US-09-492-709A-337	Sequence 337, Appl
7	31	72.1	194	2	US-09-270-767-33892	Sequence 33892, A
8	31	72.1	194	2	US-09-270-767-49109	Sequence 49109, A
9	31	72.1	303	2	US-09-248-796A-14416	Sequence 14416, A
10	31	72.1	514	2	US-09-543-681A-4255	Sequence 4255, Ap
11	30	69.8	126	2	US-09-232-290-35	Sequence 35, Appl
12	30	69.8	134	2	US-09-732-210-1742	Sequence 1742, Ap
13	30	69.8	242	2	US-09-270-767-47078	Sequence 47078, A
14	30	69.8	265	2	US-09-540-336-3285	Sequence 3285, Ap
15	30	69.8	266	2	US-09-270-767-31861	Sequence 31861, A
16	30	69.8	356	2	US-09-107-532A-4245	Sequence 4245, Ap
17	30	69.8	362	2	US-09-134-000C-3578	Sequence 3578, Ap
18	30	69.8	366	2	US-09-328-352-7292	Sequence 7292, Ap
19	30	69.8	377	2	US-09-107-532A-4318	Sequence 4318, Ap
20	30	69.8	399	2	US-09-543-681A-6125	Sequence 6125, Ap
21	30	69.8	402	2	US-09-134-001C-4138	Sequence 4138, Ap
22	30	69.8	735	2	US-08-539-205A-2	Sequence 2, Appli
23	30	69.8	735	2	US-09-392-163A-2	Sequence 2, Appli
24	30	69.8	755	2	US-09-107-532A-3693	Sequence 3693, Ap
25	30	69.8	1380	2	US-09-949-016-11688	Sequence 11688, A
26	30	69.8	1874	2	US-09-602-787A-46	Sequence 46, Appl
27	30	69.8	2777	2	US-10-220-587-4	Sequence 4, Appli

28	30	69.8	2780	2	US-10-220-587-2	Sequence 2, Appli
29	29	67.4	151	2	US-09-270-767-60568	Sequence 60568, A
30	29	67.4	168	2	US-09-270-767-42676	Sequence 42676, A
31	29	67.4	168	2	US-09-270-767-57995	Sequence 57995, A
32	29	67.4	192	2	US-09-248-796A-20050	Sequence 20050, A
33	29	67.4	229	2	US-09-763-620-17	Sequence 17, Appl
34	29	67.4	243	2	US-09-252-991A-29870	Sequence 29870, A
35	29	67.4	253	2	US-09-270-767-41859	Sequence 41859, A
36	29	67.4	290	2	US-09-002-298-9	Sequence 9, Appli
37	29	67.4	290	2	US-09-058-489-8	Sequence 8, Appli
38	29	67.4	290	2	US-09-481-277-9	Sequence 9, Appli
39	29	67.4	296	2	US-09-118-990A-5	Sequence 5, Appli
40	29	67.4	500	2	US-09-118-990A-7	Sequence 7, Appli
41	29	67.4	508	2	US-09-270-767-45071	Sequence 45071, A
42	29	67.4	521	2	US-09-270-767-43965	Sequence 43965, A
43	29	67.4	527	1	US-08-535-276-3	Sequence 3, Appli
44	29	67.4	527	2	US-09-335-234-3	Sequence 3, Appli
45	29	67.4	559	2	US-09-583-110-3735	Sequence 3735, Ap
46	29	67.4	567	2	US-09-107-433-4592	Sequence 4592, Ap
47	29	67.4	1901	2	US-09-738-946-12	Sequence 12, Appl
48	28.5	66.3	254	2	US-09-270-767-38691	Sequence 38691, A
49	28.5	66.3	254	2	US-09-270-767-53908	Sequence 53908, A
50	28	65.1	72	2	US-09-134-001C-4381	Sequence 4381, Ap
51	28	65.1	86	2	US-09-270-767-61896	Sequence 61896, A
52	28	65.1	89	2	US-09-270-767-35698	Sequence 35698, A
53	28	65.1	89	2	US-09-270-767-50915	Sequence 50915, A
54	28	65.1	106	2	US-09-513-999C-8043	Sequence 8043, Ap
55	28	65.1	138	1	US-08-698-551-4	Sequence 4, Appli
56	28	65.1	138	1	US-08-602-228-4	Sequence 4, Appli
57	28	65.1	138	1	US-08-649-341A-4	Sequence 4, Appli
58	28	65.1	138	1	US-08-494-440B-4	Sequence 4, Appli
59	28	65.1	138	1	US-08-533-901B-4	Sequence 4, Appli
60	28	65.1	138	1	US-08-839-032A-4	Sequence 4, Appli
61	28	65.1	138	1	US-08-839-031A-4	Sequence 4, Appli
62	28	65.1	138	2	US-09-185-2586-4	Sequence 4, Appli
63	28	65.1	138	2	PCT-US95-12724-1	Sequence 1500, Ap
64	28	65.1	157	2	US-09-605-703B-1500	Sequence 8633, Ap
65	28	65.1	159	2	US-09-489-039A-8633	Sequence 3438, Ap
66	28	65.1	201	2	US-09-540-236-3438	Sequence 721, App
67	28	65.1	231	2	US-09-538-092-721	Sequence 723, App
68	28	65.1	258	2	US-10-101-464A-723	Sequence 4, Appli
69	28	65.1	270	2	US-09-693-147-4	Sequence 4, Appli
70	28	65.1	280	2	US-09-489-039A-13968	Sequence 13968, A
71	28	65.1	281	2	US-09-512-251A-9	Sequence 9, Appli
72	28	65.1	281	2	US-09-515-150A-9	Sequence 12, Appl
73	28	65.1	281	2	US-09-196-281-12	Sequence 9, Appli
74	28	65.1	281	2	US-10-336-324-9	Sequence 4495, Ap
75	28	65.1	294	2	US-09-134-000C-4495	Sequence 8623, Ap
76	28	65.1	313	2	US-09-489-039A-8623	Sequence 15019, A
77	28	65.1	314	2	US-09-248-796A-15019	Sequence 46326, A
78	28	65.1	324	2	US-09-270-767-46326	Sequence 29, Appl
79	28	65.1	325	1	US-08-467-948A-29	Sequence 29, Appl
80	28	65.1	325	2	US-08-467-947A-29	Sequence 11, Appl
81	28	65.1	332	2	US-09-172-952-11	Sequence 22, Appl
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## SUMMARIES

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139	29	67.4	290	4	US-10-432-443-48	Sequence 48, Appl1	212	29	67.4	1212	4	US-10-337-963-195884	Sequence 195884, A
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142	29	67.4	290	5	US-10-972-963-74	Sequence 74, Appl1	215	29	67.4	1388	4	US-10-369-493-17749	Sequence 17749, A
143	29	67.4	290	6	US-11-019-829-91	Sequence 91, Appl1	216	29	67.4	1478	4	US-10-437-963-140834	Sequence 140834, Sequence 218, App
144	29	67.4	293	4	US-10-369-493-887	Sequence 887, App	217	28	65.1	35	4	US-10-425-115-214057	Sequence 214057, Sequence 233189, Sequence 318022, Sequence 272764, Sequence 157260, Sequence 305184, Sequence 205411, Sequence 54333, A
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154	29	67.4	395	6	US-11-097-143-24804	Sequence 24804, A	227	28	65.1	66	3	US-09-813-153-106	Sequence 106, App
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162	29	67.4	480	5	US-10-732-923-1445	Sequence 1445, Ap	235	28	65.1	99	4	US-10-425-115-263445	Sequence 263445, A
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	33	76.7	192	6	US-10-506-454-1394
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5	32	74.4	291	7	US-11-188-298-3698
6	32	74.4	751	7	US-11-052-554A-109
7	32	74.4	949	6	US-10-506-454-104
8	31	72.1	240	6	US-10-467-657-7756
9	31	72.1	3580	6	US-10-510-941-14
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12	30	69.8	428	7	US-11-188-298-20267
13	30	69.8	638	7	US-11-188-298-82067
14	30	69.8	713	7	US-11-188-298-18086
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22	29	67.4	293	7	US-11-188-298-7878
23	29	67.4	296	7	US-11-079-463-6255
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164	27	62.8	129	7	US-11-116-144-151	Sequence 151, App
165	27	62.8	129	7	US-11-116-144-151	Sequence 151, App
166	27	62.8	129	7	US-11-116-144-151	Sequence 151, App
167	27	62.8	129	7	US-11-116-144-151	Sequence 151, App
168	27	62.8	129	7	US-11-116-144-151	Sequence 151, App
169	27	62.8	129	7	US-11-116-144-151	Sequence 151, App
170	27	62.8	129	7	US-11-116-144-151	Sequence 151, App
171	27	62.8	129	7	US-11-116-144-151	Sequence 151, App



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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:40:47 ; Search time 70.5714 Seconds

(Without alignments)  
43.582 Million cell updates/sec

Title: US-10-067-484-4

Perfect score: 33  
Sequence: 1 PXXFSTRK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database :

A\_Geneseq\_21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1980s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	97.0	7	5	ABR81971 30 kDa ra
2	30	90.9	74	4	ABG11991 Novel hum
3	30	90.9	218	4	ADL04980 M. catatr
4	29	87.9	85	6	ABP80721 N. gonorr
5	29	87.9	85	6	ABP80255 N. gonorr
6	29	87.9	284	8	ADX92845 Plant ful
7	29	87.9	329	7	ADC94153 E. faeciu
8	29	87.9	358	6	ABU34617 Protein e
9	29	87.9	359	2	AAW46752 D-alanine
10	29	87.9	364	6	ABP57038 Mycobacte
11	29	87.9	369	6	ABU33822 Protein e
12	29	87.9	373	6	ABP57037 Mycobacte
13	29	87.9	373	6	ABP57039 Mycobacte
14	29	87.9	373	6	ABP57036 Mycobacte
15	29	87.9	373	6	ABM15931 Mycobacte
16	29	87.9	373	6	ABU36891 Protein e
17	29	87.9	384	6	ABU35985 Bacteri
18	29	87.9	509	7	ADP05659 Bacteri
19	29	87.9	635	7	ABR62805 Drosophi
20	28	84.8	20	5	AAW48298 Human CD4
21	28	84.8	27	5	ADK75872 Plant ful
22	28	84.8	30	5	AAW48295 Human CD4
23	28	84.8	30	5	AAW48294 Human CD4
24	28	84.8	40	4	AAW86125 Human imm

25	28	84.8	73	4	AAW17792
26	28	84.8	73	4	ABR36817
27	28	84.8	73	4	AAW30302
28	28	84.8	73	4	ABR31596
29	28	84.8	73	4	ABR22140
30	28	84.8	73	4	AAW69961
31	28	84.8	73	4	AAW57558
32	28	84.8	73	4	ABG51661
33	28	84.8	73	4	AAW05439
34	28	84.8	73	5	ABG39594
35	28	84.8	86	4	AAO12999
36	28	84.8	86	4	AAU30900
37	28	84.8	111	4	AAW63655
38	28	84.8	130	4	AAW81232
39	28	84.8	158	9	ADW93247
40	28	84.8	167	5	AAW48312
41	28	84.8	175	3	AAW55603
42	28	84.8	230	6	ABU19098
43	28	84.8	261	7	AD160182
44	28	84.8	271	3	AAW55602
45	28	84.8	271	6	ABU04648
46	28	84.8	271	6	ABU04606
47	28	84.8	273	5	AAW48308
48	28	84.8	293	6	ABU04611
49	28	84.8	294	6	ABU04624
50	28	84.8	294	6	ABU04646
51	28	84.8	303	8	ADT58684
52	28	84.8	303	8	ADK71495
53	28	84.8	338	6	ABU04649
54	28	84.8	338	6	ABU04605
55	28	84.8	359	5	AAU80862
56	28	84.8	359	5	ABU81721
57	28	84.8	360	4	AAW91204
58	28	84.8	361	2	AAW20816
59	28	84.8	361	2	AAW31444
60	28	84.8	361	2	AAW80453
61	28	84.8	361	2	AAW86200
62	28	84.8	361	3	AAW99851
63	28	84.8	361	3	AAW96139
64	28	84.8	361	4	AAU02448
65	28	84.8	361	4	ABU04622
66	28	84.8	361	6	ABU04632
67	28	84.8	361	6	ABU04643
68	28	84.8	361	6	ABU04610
69	28	84.8	361	6	ABU04638
70	28	84.8	361	6	ABU04634
71	28	84.8	361	6	ABU04626
72	28	84.8	361	6	ABU04630
73	28	84.8	361	6	ABU04609
74	28	84.8	361	6	ABU04644
75	28	84.8	361	6	ABU04607
76	28	84.8	361	6	ABU04636
77	28	84.8	361	6	AAW30338
78	28	84.8	361	7	ADD90592
79	28	84.8	361	8	ADL93508
80	28	84.8	361	8	ADW43773
81	28	84.8	361	8	ADW43385
82	28	84.8	361	8	ADW57483
83	28	84.8	361	9	ADW70207
84	28	84.8	361	9	ADW43572
85	28	84.8	361	9	ADW16699
86	28	84.8	361	9	ADW19504
87	28	84.8	361	9	AAW63870
88	28	84.8	365	9	AAW58808
89	28	84.8	370	8	ADW98805
90	28	84.8	370	8	ADW98761
91	28	84.8	395	8	ABU04615
92	28	84.8	395	8	ADW39389
93	28	84.8	425	8	ABU04617
94	28	84.8	431	4	AAW39382
95	28	84.8	431	4	AAW397650
96	28	84.8	431	6	ABU04641
97	28	84.8	436	4	AAW97651

AAW17792	Peptide #
ABR36817	Peptide #
AAW30302	Peptide #
ABR31596	Peptide #
ABR22140	Peptide #
AAW69961	Human bon
AAW57558	Human bra
ABG51661	Human liv
AAW05439	Peptide #
ABG39594	Human pep
AAO12999	Human pol
AAU30900	Novel hum
AAW63655	Human gas
AAW81232	Human hae
ADW93247	Truncated
AAW48312	Protein r
AAW55603	Arabidops
ABU19098	Protein e
AD160182	Secreted
AAW55602	Arabidops
ABU04648	Human exp
ABU04606	Human exp
AAW48308	Protein R
ABU04611	Human exp
ABU04624	Human exp
ABU04646	Human exp
ADT58684	Plant pol
ADK71495	Plant ful
ABU04649	Human exp
ABU04605	Human exp
AAU80862	Human CLA
ABU81721	Human cas
AAW91204	C glutami
AAW20816	Haemato
AAW31444	Human hae
AAW80453	Human CD4
AAW86200	Human CD4
AAW99851	Human CD4
AAW96139	Human hae
AAU02448	Human hae
ABU04622	Human exp
ABU04632	Human exp
ABU04643	Human exp
ABU04610	Human exp
ABU04638	Human exp
ABU04634	Human exp
ABU04626	Human exp
ABU04630	Human exp
ABU04609	Human exp
ABU04644	Human exp
ABU04607	Human exp
ABU04636	Human exp
AAW30338	Human CD4
ADD90592	Human CD4
ADL93508	Human CD4
ADW43773	Human CD4
ADW43385	Human myo
ADW57483	Human cel
ADW70207	Tumor-agg
ADW43572	CD4s. 4/
ADW16699	PRO polyp
ADW19504	PRO polyp
AAW63870	Protein o
AAW58808	Protein e
ADW98805	Borrelia
ADW98761	Borrelia
ABU04615	Human exp
ADW39389	Human myo
ABU04617	Human exp
ADW39382	Human myo
AAW397650	CD4Hextr
ABU04641	Human exp
AAW97651	CD4Hextr

98	28	84.8	436	6	ABU04642	ABU04642	Human exp	171	28	84.8	1024	6	ABB99643	ABb99643	Amino aci
99	28	84.8	470	6	ABU04651	ABU04651	Human exp	172	28	84.8	1061	4	ABB68826	ABb68826	Drosophil
100	28	84.8	493	2	ABU04603	ABU04603	Human exp	173	28	84.8	1070	4	AA657527	AA657527	Amino aci
101	28	84.8	493	2	AAK20817	AAK20817	Epithelia	174	28	84.8	1204	6	AAU02881	AAU02881	Human cas
102	28	84.8	493	2	AAK91445	AAK91445	Human epi	175	28	84.8	1204	6	ABG72212	ABG72212	Protein e
103	28	84.8	493	2	AAW80454	AAW80454	Human CD4	176	28	84.8	34	8	ABG72256	ABG72256	Staphyloc
104	28	84.8	493	3	AAW89151	AAW89151	Human CD4	177	27	81.8	69	5	ABE11215	ABE11215	Human ORF
105	28	84.8	493	4	AAV96140	AAV96140	Human epi	178	27	81.8	85	7	ADFO3374	ADFO3374	Bacterial
106	28	84.8	493	3	AAU02449	AAU02449	Human epi	179	27	81.8	86	4	AAU68149	AAU68149	Protonib
107	28	84.8	493	5	AAU99123	AAU99123	Haematopo	180	27	81.8	88	6	AAU52259	AAU52259	Plant full
108	28	84.8	493	6	ABU04637	ABU04637	Human exp	181	27	81.8	89	8	ADP32200	ADP32200	Human full
109	28	84.8	493	6	ABU04627	ABU04627	Human exp	182	27	81.8	91	4	ABE16731	ABE16731	Human sec
110	28	84.8	493	6	ABU04639	ABU04639	Human exp	183	27	81.8	91	7	ADP31235	ADP31235	Human nec
111	28	84.8	493	6	ABU04623	ABU04623	Human exp	184	27	81.8	106	5	ADP31235	ADP31235	Human ORF
112	28	84.8	493	6	ABU04631	ABU04631	Human exp	185	27	81.8	132	3	AAE21153	AAE21153	Human ORF
113	28	84.8	493	6	ABU04633	ABU04633	Human exp	186	27	81.8	138	3	AAE21153	AAE21153	Human ORF
114	28	84.8	493	6	ABU04612	ABU04612	Human exp	187	27	81.8	161	8	AAE21153	AAE21153	Human ORF
115	28	84.8	493	6	ABU04635	ABU04635	Human exp	188	27	81.8	161	8	AAE21153	AAE21153	Human ORF
116	28	84.8	493	6	ABU04613	ABU04613	Human exp	189	27	81.8	166	4	AAE21153	AAE21153	Human ORF
117	28	84.8	493	6	ADL93507	ADL93507	Human CD4	190	27	81.8	166	4	ADT29662	ADT29662	Human int
118	28	84.8	493	8	ADU93507	ADU93507	Human CD4	191	27	81.8	177	4	AAU30717	AAU30717	Human int
119	28	84.8	493	8	ADU93375	ADU93375	Human myo	192	27	81.8	191	4	AAU30717	AAU30717	Human int
120	28	84.8	493	8	ADU93388	ADU93388	Human CD4	193	27	81.8	259	8	ADK46373	ADK46373	Human int
121	28	84.8	518	5	AAE87764	AAE87764	Human CD4	194	27	81.8	271	6	AAU00926	AAU00926	S. pneumo
122	28	84.8	535	8	AAO17871	AAO17871	Pylin dom	195	27	81.8	271	6	AAU00926	AAU00926	S. pneumo
123	28	84.8	535	8	AAE83594	AAE83594	Human dia	196	27	81.8	285	2	AAU52270	AAU52270	H. pylori
124	28	84.8	608	8	ADP72424	ADP72424	Human myo	197	27	81.8	285	8	AAU52270	AAU52270	H. pylori
125	28	84.8	642	4	AAU25640	AAU25640	Human CD4	198	27	81.8	285	6	AAU52270	AAU52270	H. pylori
126	28	84.8	675	6	ABU04618	ABU04618	Human pro	199	27	81.8	285	6	AAU52270	AAU52270	H. pylori
127	28	84.8	676	6	ABU04602	ABU04602	Human exp	200	27	81.8	304	3	AAU52270	AAU52270	H. pylori
128	28	84.8	676	6	ABU04652	ABU04652	Human exp	201	27	81.8	310	3	AAU52270	AAU52270	H. pylori
129	28	84.8	691	8	ABU04621	ABU04621	Human exp	202	27	81.8	310	7	AAU52270	AAU52270	H. pylori
130	28	84.8	691	8	ADQ39390	ADQ39390	Human myo	203	27	81.8	310	7	AAU52270	AAU52270	H. pylori
131	28	84.8	699	6	ABU04647	ABU04647	Lung can	204	27	81.8	310	8	AAU52270	AAU52270	H. pylori
132	28	84.8	699	6	ABU04614	ABU04614	Human exp	205	27	81.8	328	2	AAU52270	AAU52270	H. pylori
133	28	84.8	699	6	ABU04614	ABU04614	Human exp	206	27	81.8	332	2	AAU52270	AAU52270	H. pylori
134	28	84.8	699	6	ABU04608	ABU04608	Human exp	207	27	81.8	339	3	AAU52270	AAU52270	H. pylori
135	28	84.8	699	7	ADU90596	ADU90596	Human CD4	208	27	81.8	339	3	AAU52270	AAU52270	H. pylori
136	28	84.8	699	9	ADU73230	ADU73230	Human col	209	27	81.8	342	3	AAU52270	AAU52270	H. pylori
137	28	84.8	699	9	ADU43570	ADU43570	Human col	210	27	81.8	361	3	AAU52270	AAU52270	H. pylori
138	28	84.8	699	9	ADU16689	ADU16689	PRO. POLYP	211	27	81.8	366	6	AAU52270	AAU52270	H. pylori
139	28	84.8	700	4	AAU97579	AAU97579	Human CD4	212	27	81.8	367	7	AAU52270	AAU52270	H. pylori
140	28	84.8	700	4	ADU04640	ADU04640	Human exp	213	27	81.8	370	7	AAU52270	AAU52270	H. pylori
141	28	84.8	700	7	ADD90594	ADD90594	Human CD4	214	27	81.8	370	9	AAU52270	AAU52270	H. pylori
142	28	84.8	700	7	ADD90594	ADD90594	Human CD4	215	27	81.8	379	9	AAU52270	AAU52270	H. pylori
143	28	84.8	719	6	ABU043568	ABU043568	Human exp	216	27	81.8	409	7	AAU52270	AAU52270	H. pylori
144	28	84.8	719	6	ABU04650	ABU04650	Human exp	217	27	81.8	416	8	AAU52270	AAU52270	H. pylori
145	28	84.8	742	4	ABU04650	ABU04650	Human exp	218	27	81.8	458	4	AAU52270	AAU52270	H. pylori
146	28	84.8	742	4	ABU04653	ABU04653	Human exp	219	27	81.8	458	7	AAU52270	AAU52270	H. pylori
147	28	84.8	742	6	ABU04620	ABU04620	Human exp	220	27	81.8	458	7	AAU52270	AAU52270	H. pylori
148	28	84.8	742	6	ABU04645	ABU04645	Human exp	221	27	81.8	459	5	AAU52270	AAU52270	H. pylori
149	28	84.8	742	7	ABU04616	ABU04616	Human exp	222	27	81.8	474	8	AAU52270	AAU52270	H. pylori
150	28	84.8	742	7	ADU95511	ADU95511	Human BRC	223	27	81.8	476	8	AAU52270	AAU52270	H. pylori
151	28	84.8	742	7	ADU95511	ADU95511	Human BRC	224	27	81.8	478	4	AAU52270	AAU52270	H. pylori
152	28	84.8	742	7	ADU95511	ADU95511	Human BRC	225	27	81.8	478	4	AAU52270	AAU52270	H. pylori
153	28	84.8	742	8	ADU95511	ADU95511	Human BRC	226	27	81.8	478	4	AAU52270	AAU52270	H. pylori
154	28	84.8	742	8	ADU95511	ADU95511	Human BRC	227	27	81.8	478	4	AAU52270	AAU52270	H. pylori
155	28	84.8	742	8	ADU95511	ADU95511	Human BRC	228	27	81.8	478	4	AAU52270	AAU52270	H. pylori
156	28	84.8	742	8	ADU95511	ADU95511	Human BRC	229	27	81.8	478	4	AAU52270	AAU52270	H. pylori
157	28	84.8	742	8	ADU95511	ADU95511	Human BRC	230	27	81.8	478	4	AAU52270	AAU52270	H. pylori
158	28	84.8	742	8	ADU95511	ADU95511	Human BRC	231	27	81.8	478	4	AAU52270	AAU52270	H. pylori
159	28	84.8	742	8	ADU95511	ADU95511	Human BRC	232	27	81.8	478	4	AAU52270	AAU52270	H. pylori
160	28	84.8	742	8	ADU95511	ADU95511	Human BRC	233	27	81.8	478	4	AAU52270	AAU52270	H. pylori
161	28	84.8	742	8	ADU95511	ADU95511	Human BRC	234	27	81.8	478	4	AAU52270	AAU52270	H. pylori
162	28	84.8	742	9	ADU95511	ADU95511	Human BRC	235	27	81.8	478	4	AAU52270	AAU52270	H. pylori
163	28	84.8	742	9	ADU95511	ADU95511	Human BRC	236	27	81.8	478	4	AAU52270	AAU52270	H. pylori
164	28	84.8	742	9	ADU95511	ADU95511	Human BRC	237	27	81.8	478	4	AAU52270	AAU52270	H. pylori
165	28	84.8	742	9	ADU95511	ADU95511	Human BRC	238	27	81.8	478	4	AAU52270	AAU52270	H. pylori
166	28	84.8	742	9	ADU95511	ADU95511	Human BRC	239	27	81.8	478	4	AAU52270	AAU52270	H. pylori
167	28	84.8	742	9	ADU95511	ADU95511	Human BRC	240	27	81.8	478	4	AAU52270	AAU52270	H. pylori
168	28	84.8	742	9	ADU95511	ADU95511	Human BRC	241	27	81.8	478	4	AAU52270	AAU52270	H. pylori
169	28	84.8	742	9	ADU95511	ADU95511	Human BRC	242	27	81.8	478	4	AAU52270	AAU52270	H. pylori
170	28	84.8	742	9	ADU95511	ADU95511	Human BRC	243	27	81.8	478	4	AAU52270	AAU52270	H. pylori

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:12 ; Search time 6.42857 Seconds  
(without alignments)  
104.769 Million cell updates/sec

Title: US-10-067-484-4

Perfect score: 33  
Sequence: 1 FYXFSRK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

1: PIR 80:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	116	2	SS0449
2	30	90.9	201	2	G64013
3	29	87.9	94	2	H69748
4	29	87.9	222	2	T30423
5	29	87.9	258	2	T45991
6	29	87.9	373	2	B70673
7	29	87.9	373	2	T34126
8	29	87.9	384	2	H87118
9	28	84.8	230	2	H70114
10	28	84.8	242	2	T16349
11	28	84.8	285	2	G72401
12	28	84.8	361	2	JH0417
13	28	84.8	395	2	I77371
14	28	84.8	426	2	JH0518
15	28	84.8	464	2	A47442
16	28	84.8	468	2	G70417
17	28	84.8	493	2	S13530
18	28	84.8	508	2	T22626
19	28	84.8	699	2	I37369
20	28	84.8	742	2	A47195
21	27	81.8	245	2	T33840
22	27	81.8	247	2	H64524
23	27	81.8	248	2	B97794
24	27	81.8	271	2	A85065
25	27	81.8	271	2	C97932
26	27	81.8	277	2	E75187
27	27	81.8	277	2	D71220
28	27	81.8	297	2	A81381
29	27	81.8	304	2	T05587

30	27	81.8	328	2	A71981
31	27	81.8	331	2	T20916
32	27	81.8	338	2	I40448
33	27	81.8	369	2	D90351
34	27	81.8	372	2	T25621
35	27	81.8	396	2	T24576
36	27	81.8	396	2	T39676
37	27	81.8	431	2	T20263
38	27	81.8	462	2	B88613
39	27	81.8	488	2	G81295
40	27	81.8	510	2	I39930
41	27	81.8	520	2	G88846
42	27	81.8	572	2	T47219
43	27	81.8	576	2	T25375
44	27	81.8	656	2	A74248
45	27	81.8	656	2	E72379
46	27	81.8	661	2	G72316
47	27	81.8	819	2	UC7240
48	27	81.8	827	1	COBYD1
49	27	81.8	835	2	JC6140
50	27	81.8	1047	2	T46599
51	27	81.8	1557	2	T28811
52	27	81.8	1770	2	A71517
53	27	81.8	2824	2	T22759
54	26	78.8	31	2	E82329
55	26	78.8	52	2	T11156
56	26	78.8	109	2	S58781
57	26	78.8	125	2	T03359
58	26	78.8	128	2	AC1150
59	26	78.8	128	2	AD1509
60	26	78.8	146	2	B95205
61	26	78.8	181	2	T23333
62	26	78.8	190	2	F97812
63	26	78.8	206	2	T35415
64	26	78.8	206	2	C83590
65	26	78.8	207	2	E69124
66	26	78.8	220	2	S44808
67	26	78.8	229	2	A37775
68	26	78.8	229	2	C82975
69	26	78.8	239	2	H82388
70	26	78.8	236	2	AI0142
71	26	78.8	250	2	T25632
72	26	78.8	253	2	A88955
73	26	78.8	264	2	B71721
74	26	78.8	266	2	D97719
75	26	78.8	272	2	T07182
76	26	78.8	287	2	H83306
77	26	78.8	309	2	D70464
78	26	78.8	318	2	T20617
79	26	78.8	360	2	T26270
80	26	78.8	364	1	CEEBDT
81	26	78.8	364	2	CEEBDA
82	26	78.8	364	2	AC0549
83	26	78.8	364	2	G90682
84	26	78.8	364	2	C85533
85	26	78.8	365	2	B70435
86	26	78.8	378	2	D83945
87	26	78.8	382	2	G86791
88	26	78.8	405	2	G86848
89	26	78.8	408	2	C95100
90	26	78.8	408	2	E97968
91	26	78.8	408	2	AE1376
92	26	78.8	408	2	AG1745
93	26	78.8	413	2	D89857
94	26	78.8	454	2	A99470
95	26	78.8	461	2	C69353
96	26	78.8	465	2	A56679
97	26	78.8	482	2	AI0554
98	26	78.8	482	2	E90688
99	26	78.8	482	2	T46944
100	26	78.8	482	2	A85539
101	26	78.8	482	2	G64771
102	26	78.8	487	1	I40654

DNA transformation  
hypothetical prote  
conserved hypotet  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable yeast cel  
hypothetical prote  
hypothetical prote  
protein T27B9.5 [1  
cytochrome-c oxida  
replication protei  
protein T12A7.2 [1  
amino acid transpo  
hypothetical prote  
methyl-accepting c  
methyl-accepting c  
methyl-accepting c  
two-pore calcium c  
RED1 protein - yea  
cell surface-assoc  
glutamate dehydrog  
hypothetical prote  
hypothetical prote  
hypothetical prote  
ATPase 8 - hardbac  
probable membrane  
gene e8 protein -  
hypothetical prote  
hypothetical prote  
conserved domain p  
hypothetical prote  
hypothetical prote  
probable transcrip  
cobalamin biosynth  
F4489.9 protein -  
phoB protein - pse  
two-component resp  
DNA-binding respon  
probable membrane  
hypothetical prote  
protein K04F1.1 [1  
probable signal pe  
signal peptidase I  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
D-alanine-D-alanin  
D-alanine-D-alanin  
D-alanine-D-alanin  
hypothetical prote  
hypothetical prote  
hypothetical prote  
conserved hypotet  
amino transferase,  
conserved hypotet  
amino transferase h  
amino transferase h  
hypothetical prote  
pyruvate dehydroge  
branched-chain ami  
probable RNA-bind  
thiamin biosynthes  
probable oxidoredu  
thiamin biosynthes  
probable oxidoredu  
virk protein - Esc  
60K inner membrane

103	26	78.8	498	2	T49064	cytochrome P450-1i
104	26	78.8	519	2	F64073	site-specific DNA-
105	26	78.8	543	2	T21143	hypothetical prote
106	26	78.8	584	2	B31767	ABC transporter (A
107	26	78.8	588	2	G84777	probable beta-fuc
108	26	78.8	601	2	T47249	nuclear envelope p
109	26	78.8	601	2	S56144	SH3 domain binding
110	26	78.8	612	2	G81750	conserved hypotet
111	26	78.8	615	2	A99105	probable ATP-depen
112	26	78.8	734	2	B70173	methionine-tRNA 1i
113	26	78.8	768	2	D11776	outer membrane pro
114	26	78.8	768	2	B97083	glycosyltransferas
115	26	78.8	894	2	T20625	hypothetical prote
116	26	78.8	932	2	F69552	leucyl-tRNA synthe
117	26	78.8	1006	2	A59384	oxycyclase/insuli
118	26	78.8	1025	2	A59383	capriccino gene pr
119	26	78.8	1058	2	T13286	hypothetical prote
120	26	78.8	1084	2	C62931	hypothetical prote
121	26	78.8	1099	2	T16882	telomerase (EC 2.7
122	26	78.8	1117	2	T14891	metabotropic gluta
123	26	78.8	1171	2	A42916	metabotropic gluta
124	26	78.8	1180	2	JC2132	DNA-directed RNA p
125	26	78.8	1212	2	JC2131	cytochrome link
126	26	78.8	1227	2	T50384	hypothetical prote
127	26	78.8	1246	2	T25284	complement compone
128	26	78.8	1346	2	T14074	hypothetical prote
129	26	78.8	1380	2	T2894	extracellular hemo
130	26	78.8	1394	2	C64474	hypothetical prote
131	26	78.8	1407	2	S50516	hypothetical prote
132	26	75.8	107	2	A71172	phenotypic variati
133	26	75.8	141	2	A13330	probable N-acetyl
134	26	75.8	144	2	A60334	disease resistance
135	26	75.8	147	2	D83586	hypothetical prote
136	26	75.8	158	2	T06433	probable tetra-fam1
137	26	75.8	184	2	S12393	transcription regu
138	26	75.8	188	2	T33738	conserved hypotet
139	26	75.8	195	2	B86814	guia protein homol
140	26	75.8	208	2	A75254	hypothetical prote
141	26	75.8	247	2	E75052	hypothetical prote
142	26	75.8	254	2	T05864	hypothetical prote
143	26	75.8	274	2	T34282	ABC transporter, p
144	26	75.8	281	2	G95196	glucokinase (impor
145	26	75.8	294	2	D98063	ROR family protei
146	26	75.8	294	2	F98061	hypothetical prote
147	26	75.8	294	2	A95195	D-alanine-D-alanin
148	26	75.8	311	2	B70083	hypothetical prote
149	26	75.8	311	2	E97741	D-alanine-D-alanin
150	26	75.8	321	2	E71679	hypothetical prote
151	26	75.8	321	2	T29419	hypothetical prote
152	26	75.8	329	2	B6456	2,4-dienoyl-CoA re
153	26	75.8	335	2	S11021	D-alanine-D-alanin
154	26	75.8	335	2	D75529	D-alanine-D-alanin
155	26	75.8	339	2	S77119	D-alanyl-D-alanin
156	26	75.8	354	2	A11928	hypothetical prote
157	26	75.8	364	2	T16376	hypothetical prote
158	26	75.8	368	2	T47445	uncharacterized pr
159	26	75.8	371	2	C97355	hypothetical prote
160	26	75.8	379	2	D84742	probable carrier p
161	26	75.8	384	1	S44092	multidrug resistan
162	26	75.8	395	2	S39659	multidrug resistan
163	26	75.8	419	2	AG1660	dicarboxylic acid
164	26	75.8	419	2	AH1288	alpha-ketoglutarat
165	26	75.8	432	2	A83616	alpha-ketoglutarat
166	26	75.8	432	2	D85905	alpha-ketoglutarat
167	26	75.8	432	2	F91060	hypothetical prote
168	26	75.8	432	2	H64514	hypothetical prote
169	26	75.8	432	2	AG0831	alpha-ketoglutarat
170	26	75.8	433	2	E82848	hypothetical prote
171	26	75.8	435	2	T33246	alpha-ketoglutarat
172	26	75.8	442	2	AF3321	toxlin-A - jellyfis
173	26	75.8	457	2	JC7372	
174	26	75.8	463	2		
175	26	75.8	463	2		
176	25	75.8	466	2	D84906	probable beta-keto
177	25	75.8	472	2	T35662	probable sugar tra
178	25	75.8	504	2	T45422	glutamyl-tRNA synt
179	25	75.8	504	2	T29338	hypothetical prote
180	25	75.8	528	2	H70140	oligopeptidase abc
181	25	75.8	536	2	T24218	hypothetical prote
182	25	75.8	607	2	F64227	DNA primase (dnaB)
183	25	75.8	628	1	A40802	protein-tyrosine k
184	25	75.8	635	1	I48781	protein-tyrosine k
185	25	75.8	635	1	A53596	protein-tyrosine k
186	25	75.8	646	2	T32269	hypothetical prote
187	25	75.8	646	2	G69871	hypothetical prote
188	25	75.8	725	2	AG1802	maltoase phosphoryl
189	25	75.8	753	2	S22802	transposase (clone
190	25	75.8	768	2	B97725	transposase (clone
191	25	75.8	800	2	C89911	topoisomerase IV s
192	25	75.8	800	2	S54427	gyrase-like protei
193	25	75.8	800	2	T09499	ATP-dependent clip
194	25	75.8	1010	2	JC1266	beta-galactosidase
195	25	75.8	1025	1	F95141	type II site-speci
196	25	75.8	1084	2	D98009	type II site-speci
197	25	75.8	1442	2	S57160	sulfite reductase
198	25	75.8	1487	2	H81263	glutamate synthase
199	25	75.8	50	2	B84370	repa protein homol
200	24	72.7	63	2	S76589	hypothetical prote
201	24	72.7	70	2	S76589	hypothetical prote
202	24	72.7	98	2	PQ0372	hypothetical prote
203	24	72.7	101	2	D75013	60S ribosomal prot
204	24	72.7	106	2	G90016	hypothetical prote
205	24	72.7	116	2	B71702	ribosome-binding f
206	24	72.7	128	2	T28585	15R protein - Var
207	24	72.7	139	2	D72169	A44R protein - Var
208	24	72.7	139	2	I36852	flagellar protein
209	24	72.7	139	2	B70049	phage hypotetralin
210	24	72.7	140	2	A10276	hypothetical prote
211	24	72.7	143	2	C86646	hypothetical prote
212	24	72.7	159	2	A87299	acetyltransferase,
213	24	72.7	159	2	A81371	probable acetyltra
214	24	72.7	162	2	S38597	hypothetical prote
215	24	72.7	162	2	AB1950	hypothetical prote
216	24	72.7	168	2	AB1950	conserved hypotet
217	24	72.7	168	2	G89830	hypothetical prote
218	24	72.7	168	2	H69476	transcriptional regu
219	24	72.7	169	2	H95049	hypothetical prote
220	24	72.7	172	2	H86211	protein P2489.22 l
221	24	72.7	179	2	C82441	hypothetical prote
222	24	72.7	187	2	A90126	conserved hypotet
223	24	72.7	195	2	T09743	myb-related protei
224	24	72.7	198	2	S43593	conserved hypotet
225	24	72.7	200	2	H71639	NADH2 dehydrogenas
226	24	72.7	205	2	H97882	transcription regu
227	24	72.7	205	2	T01153	probable seed manu
228	24	72.7	206	2	AD3195	hypothetical prote
229	24	72.7	207	2	T25237	alkyl hydroperoxid
230	24	72.7	211	2	A99370	hypothetical prote
231	24	72.7	212	2	E72047	hypothetical prote
232	24	72.7	215	2	D86576	conserved hypotet
233	24	72.7	217	2	AP2769	transcription regu
234	24	72.7	220	2	G97549	probable transcrip
235	24	72.7	222	2	AE1867	hypothetical prote
236	24	72.7	222	2	AE2191	hypothetical prote
237	24	72.7	222	2	T40315	hypothetical prote
238	24	72.7	224	2	BVECTJ	trna protein - Bsc
239	24	72.7	229	1	B77829	probable transcrip
240	24	72.7	232	2	B64667	purine-nucleoside
241	24	72.7	232	2	C71848	hypothetical prote
242	24	72.7	233	2	T08402	hypothetical prote
243	24	72.7	235	2	T24759	C-8 sterol isomera
244	24	72.7	237	2	T46871	hypothetical prote
245	24	72.7	256	2	AD1115	
246	24	72.7	256	2		
247	24	72.7	257	2		
248	24	72.7	257	2	T35018	

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:05 ; Search time 38.1429 Seconds  
(without alignments)  
129.479 Million cell updates/sec

Title: US-10-067-484-4

Perfect score: 33  
Sequence: 1 FXXFSTK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	41	2	091FZ4 IRV6
2	32	97.0	108	2	06B6C0 CAMJE
3	32	97.0	281	2	061VH7 CAEBR
4	32	97.0	416	2	04HD92 CAMCO
5	32	97.0	615	2	081JDP PLAF7
6	32	97.0	1751	2	054T12 DICDI
7	30	90.9	60	2	08F8P3 LBPIN
8	30	90.9	116	1	YEB0_YEAST
9	30	90.9	199	2	087NM8 VIBPA
10	30	90.9	201	1	Y787_HABIN
11	30	90.9	207	2	04QWB2 HAE18
12	30	90.9	473	2	0600W4 MYCHY
13	30	90.9	477	2	0642R1 XENIA
14	30	90.9	623	2	0517H8_ENTHI
15	29	87.9	30	2	041PV1 PLABE
16	29	87.9	94	1	YBFE_BACSU
17	29	87.9	100	2	065XA7 ORYSA
18	29	87.9	129	2	041450 STAHJ
19	29	87.9	202	2	061PY2 PHOHR
20	29	87.9	207	2	063BG4_BACCZ
21	29	87.9	209	2	050SE7_ENTHI
22	29	87.9	209	2	05NT08_ENTHI
23	29	87.9	209	2	06HIX3_BACCH
24	29	87.9	209	2	081OL8_BACAN
25	29	87.9	222	2	09YMO2_NPVLD
26	29	87.9	224	2	08VSW2_STAXY
27	29	87.9	227	2	06SX64_HCMV
28	29	87.9	227	2	06SX85_HCMV
29	29	87.9	258	1	UPPS_THEAC
30	29	87.9	258	1	UPPS_THEVO
31	29	87.9	258	2	Q9M2T5_ARATH

32	29	87.9	258	2	Q6MEF4_PARUW	Q6MEF4_parchlamyd
33	29	87.9	262	2	Q863X2_PIG	Q863X2_sus scrofa
34	29	87.9	297	2	Q8AV24_FUGRU	Q8AV24_fugu rubrip
35	29	87.9	339	2	Q60ZM4_CAEBR	Q60ZM4_caenorhabdi
36	29	87.9	348	2	Q75D24_ASHGO	Q75D24_ashya goss
37	29	87.9	369	2	Q73VU4_MYCPA	Q73VU4_mycobacteri
38	29	87.9	370	1	DDL_MYCBO	Q7CX19_mycobacteri
39	29	87.9	373	1	DDL_MYCSM	Q9ZG10_mycobacteri
40	29	87.9	373	1	DDL_MYCTU	P95114_mycobacteri
41	29	87.9	373	1	Q18197_CAEBL	Q18197_caenorhabdi
42	29	87.9	384	1	DDL_MYCLE	Q9CB60_mycobacteri
43	29	87.9	491	1	ZAPR_PROMI	Q11137_proteus mir
44	29	87.9	491	1	Q85374_PROMI	Q85374_proteus mir
45	29	87.9	555	2	Q51AD3_BACER	Q51AD3_bacteroides
46	29	87.9	555	2	Q64OR5_BACPR	Q64OR5_bacteroides
47	29	87.9	635	2	Q9VUK7_DROME	Q9VUK7_drosophila
48	29	87.9	700	2	Q720Z1_LISNF	Q720Z1_listeria mo
49	29	87.9	1251	2	Q4YV48_PLABE	Q4YV48_plasmodium
50	29	87.9	1319	2	Q61EX3_CAEBR	Q61EX3_caenorhabdi
51	29	87.9	1435	2	Q7S924_NEUCR	Q7S924_neutrospora
52	29	87.9	1435	2	Q7RTC8_PLAVO	Q7RTC8_plasmodium
53	29	87.9	1976	2	Q7YH13_RHOBR	Q7YH13_rhodnius pr
54	29	87.9	1976	2	Q6Z103_ORYSA	Q6Z103_oryza sativ
55	29	87.9	188	2	Q6ME93_PARUW	Q6ME93_parchlamyd
56	29	87.9	173	2	Q4PED0_USTWA	Q4PED0_ustilago ma
57	29	87.9	188	2	Q4SWW5_TETVG	Q4SWW5_tetradodon n
58	29	87.9	207	2	Q8UP61_9H1Y1	Q8UP61_human immun
59	29	87.9	224	2	Q631P1_BURPS	Q631P1_burkholderi
60	29	87.9	226	2	Q4UIR4_RICER	Q4UIR4_rickettsia
61	29	87.9	229	2	Q8VS70_BORHE	Q8VS70_borrelia he
62	29	87.9	230	1	UPPS_BORBU	Q51146_borrelia bu
63	29	87.9	230	1	Q662P2_BORCA	Q662P2_borrelia ga
64	29	87.9	230	2	Q6KH6C_MYCMO	Q6KH6C_mycoplasma
65	29	87.9	236	2	Q9T241_PHYTN	Q9T241_phytophthor
66	29	87.9	236	2	Q52VA3_PHTYN	Q52VA3_homo sapien
67	29	87.9	211	2	Q9HSA3_HUMAN	Q9HSA3_homo sapien
68	29	87.9	285	2	Q9WY71_THENA	Q9WY71_thermoga
69	29	87.9	285	2	Q92493_HUMAN	Q92493_homo sapien
70	29	87.9	308	2	Q81J10_PLAF7	Q81J10_plasmodium
71	29	87.9	309	2	Q97308_PLAF7	Q97308_plasmodium
72	29	87.9	309	2	Q6LEW0_PLAF7	Q6LEW0_plasmodium
73	29	87.9	312	2	Q6SFP9_9BACT	Q6SFP9_uncultured
74	29	87.9	337	2	Q60M40_CAEBR	Q60M40_caenorhabdi
75	29	87.9	338	2	Q9H5A4_HUMAN	Q9H5A4_homo sapien
76	29	87.9	354	2	Q91RS0_GVCP	Q91RS0_cydia pomon
77	29	87.9	358	2	Q7PA00_FUSNV	Q7PA00_fusobacteri
78	29	87.9	359	2	Q5TMS2_ANOCA	Q5TMS2_anopheles g
79	29	87.9	360	1	DDL_CORGL	Q8FPG9_corynebacte
80	29	87.9	361	1	DDL_CORGL	Q8FPG9_corynebacte
81	29	87.9	361	2	Q86T72_HUMAN	Q86T72_homo sapien
82	29	87.9	361	2	Q8N694_HUMAN	Q8N694_homo sapien
83	29	87.9	362	2	Q9S051_BORBU	Q9S051_borrelia bu
84	29	87.9	363	2	Q5YH77_NOCFA	Q5YH77_nocardia fa
85	29	87.9	365	2	Q6NHK6_CORB1	Q6NHK6_corynebacte
86	29	87.9	368	2	Q86G14_TOXOQ	Q86G14_tetoxoplasma
87	29	87.9	370	2	Q5XYW3_BORCA	Q5XYW3_borrelia ga
88	29	87.9	370	2	Q9R2W7_BORBU	Q9R2W7_borrelia bu
89	29	87.9	370	2	Q9S003_BORBU	Q9S003_borrelia bu
90	29	87.9	370	2	Q9S096_BORBU	Q9S096_borrelia bu
91	29	87.9	370	2	Q9S0C8_BORBU	Q9S0C8_borrelia bu
92	29	87.9	370	2	Q9S0F9_BORBU	Q9S0F9_borrelia bu
93	29	87.9	373	2	Q5XZ68_BORCA	Q5XZ68_borrelia ga
94	29	87.9	373	2	Q61RV3_PHOBR	Q61RV3_photobacter
95	29	87.9	375	2	Q8XJ73_CLOPE	Q8XJ73_clostridium
96	29	87.9	380	2	Q4XFR0_PLACH	Q4XFR0_plasmodium
97	29	87.9	384	2	Q6Z8A1_CAEBR	Q6Z8A1_caenorhabdi
98	29	87.9	390	2	Q8PG20_XANAC	Q8PG20_xanthomonas
99	29	87.9	407	2	Q9N3V7_CAEBL	Q9N3V7_caenorhabdi
100	29	87.9	412	2	Q87P22_VIBPA	Q87P22_vibrio para
101	29	87.9	423	2	Q5H3V1_XANOR	Q5H3V1_xanthomonas
102	29	87.9	441	2	Q8WTM2_CAEBL	Q8WTM2_caenorhabdi
103	29	87.9	443	2	Q8A9Y4_BACIN	Q8A9Y4_bacteroides
104	29	87.9	446	2	Q7T2X4_ONCMY	Q7T2X4_oncorhynchu

105	28	84.8	452	2	062YN6	BRABE	062YN6	brachydanio	178	27	81.8	271	2	08DYO	STRB6	08DYU0	streptococc
106	28	84.8	458	2	05ORV7	ENTHI	05ORV7	entameoba h	179	27	81.8	271	2	07D55	STRB6	07D55	streptococc
107	28	84.8	464	1	OLEM	RANCA	007081	rana catesbe	180	27	81.8	275	2	07D55	ASBHO	07D55	asbho goss
108	28	84.8	468	2	067370	AQUAE	067370	aquifex aeo	181	27	81.8	277	2	07D57	EXRNO	07D57	exrno
109	28	84.8	470	2	09H546	HUMAN	09H566	homo saplen	182	27	81.8	277	2	08TX1	PYRAB	08TX1	pyrococcus
110	28	84.8	493	2	066227	HUMAN	066227	homo saplen	183	27	81.8	277	2	08TX1	STRAC	08TX1	pyrococcus
111	28	84.8	493	2	05R9V4	PONPY	05R9V4	pongo pygma	184	27	81.8	286	2	02CD3	STRAC	02CD3	staphylococ
112	28	84.8	493	2	05R9V4	PONPY	05R9V4	pongo pygma	185	27	81.8	286	2	02CD3	STRAC	02CD3	staphylococ
113	28	84.8	517	1	NAS28	CAEEL	P86061	caenorhabdi	186	27	81.8	291	2	05DPA2	ENTHI	05DPA2	entameoba h
114	28	84.8	520	2	062913	RAT	062913	rattus norv	187	27	81.8	291	2	05DPA2	ENTHI	05DPA2	entameoba h
115	28	84.8	557	2	05AC27	CANAL	05AC27	canidia alb	188	27	81.8	297	1	08M6X4	GNBOP	08M6X4	gnbop
116	28	84.8	557	2	07NBUS	MYCAG	07NBUS	mycoplasma	189	27	81.8	297	1	04HFR4	CAMCO	04HFR4	campylobact
117	28	84.8	576	2	06ARY5	DESPS	06ARY5	desulfohalo	190	27	81.8	297	1	04HFR4	CAMCO	04HFR4	campylobact
118	28	84.8	591	2	05SG60	ENTHI	05SG60	entamoeba h	191	27	81.8	297	1	04HFR4	CAMCO	04HFR4	campylobact
119	28	84.8	613	2	05ZJ91	CHICK	05ZJ91	gallus gall	192	27	81.8	297	1	04HFR4	CAMCO	04HFR4	campylobact
120	28	84.8	676	2	05H5A7	HUMAN	05H5A7	homo saplen	193	27	81.8	304	1	05HW88	CAMTR	05HW88	campylobact
121	28	84.8	715	2	05CRU3	CRYPV	05CRU3	cryptospori	194	27	81.8	304	1	05HW88	CAMTR	05HW88	campylobact
122	28	84.8	717	2	05H5A5	HUMAN	05H5A5	homo saplen	195	27	81.8	311	2	08FVNB	MOUSE	08FVNB	mesophilic
123	28	84.8	742	1	CP44	HUMAN	P16070	h cd4 anti	196	27	81.8	318	2	08FVNB	MOUSE	08FVNB	mesophilic
124	28	84.8	742	1	CP44	HUMAN	P16070	h cd4 anti	197	27	81.8	318	2	08FVNB	MOUSE	08FVNB	mesophilic
125	28	84.8	878	2	09UJ36	HUMAN	09UJ36	homo saplen	198	27	81.8	321	2	08FVNB	MOUSE	08FVNB	mesophilic
126	28	84.8	878	2	09UJ36	HUMAN	09UJ36	homo saplen	199	27	81.8	321	2	08FVNB	MOUSE	08FVNB	mesophilic
127	28	84.8	1004	2	QJ3K22	TREDE	QJ3K22	treponema d	200	27	81.8	322	2	07ROZ2	ANOGA	07ROZ2	anophelis g
128	28	84.8	1024	1	CAR12	HUMAN	QJ3K22	treponema d	201	27	81.8	322	2	07ROZ2	ANOGA	07ROZ2	anophelis g
129	28	84.8	1061	2	QVXH9	DRONE	QVXH9	homo saplen	202	27	81.8	326	2	05T257	BRABE	05T257	brachydanio
130	28	84.8	1221	2	Q7O139	LOTDA	Q7O139	lotus japon	203	27	81.8	328	2	09ZKX5	HELPI	09ZKX5	hellicobacte
131	28	84.8	1446	2	Q4MTH8	THEPA	Q4MTH8	thelateria p	204	27	81.8	329	2	06HN67	BACEL	06HN67	bacellus th
132	28	84.8	3064	2	Q4MTH8	THEPA	Q4MTH8	thelateria p	205	27	81.8	331	2	08HN67	BACEL	08HN67	bacellus th
133	28	84.8	3064	2	Q4MTH8	THEPA	Q4MTH8	thelateria p	206	27	81.8	331	2	08HN67	BACEL	08HN67	bacellus th
134	27	81.8	38	2	Q5CUC1	SCHOA	Q5CUC1	schistosoma	207	27	81.8	332	2	08HN67	BACEL	08HN67	bacellus th
135	27	81.8	43	2	Q4MTH8	THEPA	Q4MTH8	thelateria p	208	27	81.8	332	2	08HN67	BACEL	08HN67	bacellus th
136	27	81.8	72	2	Q4MTH8	THEPA	Q4MTH8	thelateria p	209	27	81.8	334	2	06IM03	BACBR	06IM03	bacillus ce
137	27	81.8	103	2	Q4MTH8	THEPA	Q4MTH8	thelateria p	210	27	81.8	335	2	04RFX5	TETNG	04RFX5	tetraglo
138	27	81.8	110	2	Q4MTH8	THEPA	Q4MTH8	thelateria p	211	27	81.8	338	1	07S09	MOUSE	07S09	mouse
139	27	81.8	116	2	Q4MTH8	THEPA	Q4MTH8	thelateria p	212	27	81.8	347	2	05H614	XANOR	05H614	xanthomonas
140	27	81.8	122	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	213	27	81.8	354	2	093967	9FIRM	093967	desulfotoba
141	27	81.8	128	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	214	27	81.8	356	2	09KIS1	CAMJE	09KIS1	campylobact
142	27	81.8	140	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	215	27	81.8	357	2	08IB05	BACBR	08IB05	bacillus ce
143	27	81.8	140	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	216	27	81.8	357	2	08IB05	BACBR	08IB05	bacillus ce
144	27	81.8	144	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	217	27	81.8	357	2	08IB05	BACBR	08IB05	bacillus ce
145	27	81.8	146	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	218	27	81.8	357	2	08IB05	BACBR	08IB05	bacillus ce
146	27	81.8	146	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	219	27	81.8	357	2	08IB05	BACBR	08IB05	bacillus ce
147	27	81.8	150	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	220	27	81.8	360	2	08IB05	BACBR	08IB05	bacillus ce
148	27	81.8	150	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	221	27	81.8	363	2	08IB05	BACBR	08IB05	bacillus ce
149	27	81.8	152	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	222	27	81.8	366	2	08IB05	BACBR	08IB05	bacillus ce
150	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	223	27	81.8	391	2	05ML02	BACSK	05ML02	bacillus su
151	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	224	27	81.8	396	2	022250	CAEEL	022250	caenorhabdi
152	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	225	27	81.8	407	2	061ZV3	CABER	061ZV3	caenorhabdi
153	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	226	27	81.8	409	2	04UB18	THEAN	04UB18	thelateria a
154	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	227	27	81.8	409	2	04UB18	THEAN	04UB18	thelateria a
155	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	228	27	81.8	412	2	07ML11	VIBVU	07ML11	vibrio vuln
156	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	229	27	81.8	416	2	07ML11	VIBVU	07ML11	vibrio vuln
157	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	230	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
158	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	231	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
159	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	232	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
160	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	233	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
161	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	234	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
162	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	235	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
163	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	236	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
164	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	237	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
165	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	238	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
166	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	239	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
167	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	240	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
168	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	241	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
169	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	242	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
170	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	243	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
171	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	244	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
172	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	245	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
173	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	246	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
174	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	247	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
175	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	248	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
176	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	249	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas
177	27	81.8	154	2	QVQ6N1	HELPI	QVQ6N1	hellicobacte	250	27	81.8	433	2	08KNS8	PESEB	08KNS8	peseudomonas

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OM protein - protein search, using SW model

Run on: April 18, 2006, 10:41:21 ; Search time 13.5714 Seconds  
(without alignments)  
42.643 Million cell updates/sec

Title: US-10-067-484-4  
Perfect score: 33  
Sequence: 1 FXXFSTK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5 COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/6 COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/R COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/PCRTUS COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/RB COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	218	2	US-09-540-236-2666 Sequence 2666, Ap
2	29	87.9	63	2	US-09-248-796A-24322 Sequence 24322, A
3	29	87.9	329	2	US-09-107-532A-3780 Sequence 3780, Ap
4	29	87.9	509	2	US-09-543-681A-5944 Sequence 5944, Ap
5	28	84.8	177	2	US-08-938-669A-30 Sequence 30, Appl
6	28	84.8	177	2	US-09-306-828-30 Sequence 30, Appl
7	28	84.8	295	2	US-09-949-016-9143 Sequence 9143, Ap
8	28	84.8	361	1	US-07-946-497-6 Sequence 6, Appl
9	28	84.8	361	1	US-08-483-322-6 Sequence 6, Appl
10	28	84.8	361	1	US-08-478-882-6 Sequence 5968, Ap
11	28	84.8	361	1	US-09-949-016-5968 Sequence 3, Appl
12	28	84.8	464	1	US-09-021-323-3 Sequence 3, Appl
13	28	84.8	573	2	US-09-248-796A-15753 Sequence 15753, A
14	28	84.8	898	2	US-10-449-315-11 Sequence 11, Appl
15	28	84.8	1024	2	US-10-449-315-2 Sequence 2, Appl
16	28	84.8	1204	2	US-10-449-315-5 Sequence 5, Appl
17	27	81.8	75	2	US-09-248-796A-17035 Sequence 17035, A
18	27	81.8	85	2	US-09-543-681A-5659 Sequence 5659, Ap
19	27	81.8	259	2	US-09-583-110-2888 Sequence 2888, Ap
20	27	81.8	285	2	US-09-107-433-4723 Sequence 4723, Ap
21	27	81.8	356	2	US-09-270-767-37087 Sequence 37087, A
22	27	81.8	356	2	US-09-270-767-52304 Sequence 52304, A
23	27	81.8	367	2	US-09-543-681A-4571 Sequence 4571, Ap
24	27	81.8	487	2	US-09-620-412C-349 Sequence 349, App
25	27	81.8	501	2	US-09-598-419-349 Sequence 1806, A
26	27	81.8	585	2	US-09-489-039A-13806 Sequence 6426, Ap
27	27	81.8	585	2	US-09-328-352-6426 Sequence 6426, Ap

28	27	81.8	821	2	US-09-556-877-195 Sequence 195, App
29	27	81.8	821	2	US-09-620-412C-195 Sequence 195, App
30	27	81.8	821	2	US-09-598-419-195 Sequence 195, App
31	27	81.8	1419	2	US-10-197-220-173 Sequence 173, App
32	27	81.8	1776	2	US-09-556-877-179 Sequence 179, App
33	27	81.8	1776	2	US-09-620-412C-179 Sequence 179, App
34	27	81.8	1776	2	US-09-598-419-179 Sequence 23391, A
35	26	78.8	213	2	US-09-252-991A-24015 Sequence 24015, A
36	26	78.8	263	2	US-09-252-991A-24015 Sequence 19955, A
37	26	78.8	268	2	US-09-248-796A-19955 Sequence 2, Appl
38	26	78.8	291	2	US-10-083-624-2 Sequence 2, Appl
39	26	78.8	310	2	US-09-543-681A-6858 Sequence 31493, A
40	26	78.8	324	2	US-09-252-991A-31493 Sequence 18164, A
41	26	78.8	331	2	US-09-248-796A-18164 Sequence 9, Appl
42	26	78.8	364	1	US-08-454-196-9 Sequence 10, Appl
43	26	78.8	364	1	US-08-454-196-10 Sequence 32, Appl
44	26	78.8	364	1	US-08-286-819A-32 Sequence 32, Appl
45	26	78.8	364	2	US-08-980-357-32 Sequence 9, Appl
46	26	78.8	364	2	US-09-064-033-9 Sequence 10, Appl
47	26	78.8	364	2	US-09-064-033-10 Sequence 9, Appl
48	26	78.8	364	2	US-09-291-046-9 Sequence 10, Appl
49	26	78.8	364	2	US-09-291-046-10 Sequence 32, Appl
50	26	78.8	364	2	US-09-357-375-32 Sequence 12995, A
51	26	78.8	389	2	US-09-489-039A-12995 Sequence 5062, Ap
52	26	78.8	408	2	US-09-583-110-5062 Sequence 5375, A
53	26	78.8	416	2	US-09-134-000C-5375 Sequence 2664, Ap
54	26	78.8	423	2	US-09-107-433-2664 Sequence 4879, Ap
55	26	78.8	428	2	US-09-134-001C-4879 Sequence 7, Appl
56	26	78.8	438	2	US-09-906-408A-7 Sequence 20, Appl
57	26	78.8	458	2	US-09-991-181-20 Sequence 20, Appl
58	26	78.8	458	2	US-09-990-444-20 Sequence 20, Appl
59	26	78.8	458	2	US-09-997-333-20 Sequence 20, Appl
60	26	78.8	458	2	US-09-992-598-20 Sequence 12993, A
61	26	78.8	493	2	US-09-489-039A-12993 Sequence 3493, Ap
62	26	78.8	543	2	US-10-104-042-3493 Sequence 6455, Ap
63	26	78.8	674	2	US-09-328-352-6455 Sequence 8, Appl
64	26	78.8	866	1	US-08-386-727-8 Sequence 8, Appl
65	26	78.8	866	1	US-08-600-452A-8 Sequence 12, Appl
66	26	78.8	877	1	US-08-072-574-12 Sequence 12, Appl
67	26	78.8	877	1	US-08-486-270-12 Sequence 12, Appl
68	26	78.8	877	2	US-08-367-264-12 Sequence 12, Appl
69	26	78.8	877	2	US-09-153-757-12 Sequence 12, Appl
70	26	78.8	877	2	US-09-459-715-12 Sequence 2, Appl
71	26	78.8	942	2	US-09-695-481-2 Sequence 4, Appl
72	26	78.8	975	2	US-09-695-481-4 Sequence 6, Appl
73	26	78.8	1043	2	US-09-695-481-6 Sequence 8, Appl
74	26	78.8	1180	1	US-08-072-574-8 Sequence 8, Appl
75	26	78.8	1180	1	US-08-486-270-8 Sequence 8, Appl
76	26	78.8	1180	2	US-08-367-264-8 Sequence 2, Appl
77	26	78.8	1180	2	US-08-660-148-2 Sequence 8, Appl
78	26	78.8	1180	2	US-09-153-757-8 Sequence 8, Appl
79	26	78.8	1180	2	US-09-459-715-8 Sequence 10, Appl
80	26	78.8	1212	1	US-08-072-574-10 Sequence 10, Appl
81	26	78.8	1212	1	US-08-486-270-10 Sequence 10, Appl
82	26	78.8	1212	2	US-08-367-264-10 Sequence 5, Appl
83	26	78.8	1212	2	US-08-660-148-5 Sequence 10, Appl
84	26	78.8	1212	2	US-09-153-757-10 Sequence 10, Appl
85	26	78.8	1212	2	US-09-459-715-10 Sequence 7, Appl
86	26	78.8	1212	2	US-09-695-481-7 Sequence 4, Appl
87	26	78.8	1311	1	US-08-540-406-4 Sequence 4, Appl
88	26	78.8	1311	1	US-08-656-055-4 Sequence 4, Appl
89	26	78.8	1311	2	US-08-954-668-4 Sequence 4, Appl
90	26	78.8	1311	2	US-08-954-668-4 Sequence 4, Appl
91	26	78.8	1311	2	US-09-724-631-4 Sequence 4, Appl
92	26	78.8	1311	2	US-08-954-668-4 Sequence 4, Appl
93	26	78.8	1311	2	US-09-754-032-4 Sequence 4, Appl
94	26	78.8	1311	2	US-08-916-140-4 Sequence 4, Appl
95	26	78.8	1311	4	PCT-US95-13233-4 Sequence 10, Appl
96	25	75.8	40	2	US-08-963-891A-20475 Sequence 20475, A
97	25	75.8	65	2	US-09-252-991A-20475 Sequence 4523, Ap
98	25	75.8	69	2	US-09-583-110-4523 Sequence 16, Appl
99	25	75.8	69	2	US-09-107-433-4523 Sequence 16, Appl
100	25	75.8	70	1	US-08-222-616-6 Sequence 16, Appl



101	25	75.8	70	2	US-08-446-648-16	Sequence 16, Appl	174	24	72.7	86	2	US-09-543-661A-8011	Sequence 8011, Ap
102	25	75.8	70	2	US-09-982-610-16	Sequence 16, Appl	175	24	72.7	91	2	US-09-248-796A-22067	Sequence 22067, A
103	25	75.8	70	4	PCT-US95-04228-16	Sequence 16, Appl	176	24	72.7	94	2	US-09-248-796A-21486	Sequence 21486, A
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110	28	84.8	642	5	US-10-296-115-1155	Sequence 1155, Ap	183	27	81.8	157	4	US-10-225-068-176	Sequence 176, App
111	28	84.8	675	5	US-10-473-127-1184	Sequence 1284, Ap	184	27	81.8	158	4	US-10-525-068A-664	Sequence 925, App
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113	28	84.8	676	5	US-10-473-127-1318	Sequence 1318, Ap	186	27	81.8	160	4	US-10-225-068-176	Sequence 176, App
114	28	84.8	691	4	US-10-741-601-344	Sequence 344, App	187	27	81.8	161	5	US-10-225-068A-664	Sequence 664, App
115	28	84.8	691	5	US-10-473-127-1287	Sequence 1287, Ap	188	27	81.8	162	5	US-10-774-355A-1819	Sequence 1819, Ap
116	28	84.8	691	5	US-10-471-600-1053	Sequence 1053, Ap	189	27	81.8	163	5	US-10-774-355A-2531	Sequence 2531, Ap
117	28	84.8	699	5	US-10-473-127-1274	Sequence 1274, Ap	190	27	81.8	164	5	US-10-774-355A-2530	Sequence 2530, Ap
118	28	84.8	699	5	US-10-473-127-1280	Sequence 1280, Ap	191	27	81.8	165	5	US-10-335-977-8813	Sequence 8813, App
119	28	84.8	699	5	US-10-473-127-1313	Sequence 1313, Ap	192	27	81.8	166	3	US-09-740-668A-28	Sequence 687, App
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123	28	84.8	700	5	US-10-473-127-1306	Sequence 1306, Ap	196	27	81.8	170	4	US-10-425-114-50100	Sequence 50100, A
124	28	84.8	700	5	US-10-505-769-4	Sequence 4, Appl1	197	27	81.8	171	4	US-10-424-599-442895	Sequence 247895,
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128	28	84.8	742	4	US-10-116-275-206	Sequence 206, App	201	27	81.8	175	4	US-10-108-260A-3319	Sequence 3319, App
129	28	84.8	742	4	US-10-648-593-176	Sequence 176, App	202	27	81.8	176	4	US-10-112-944-401	Sequence 401, App
130	28	84.8	742	4	US-10-663-244-1	Sequence 1, Appl1	203	27	81.8	177	4	US-11-048-692-2	Sequence 2, Appl1
131	28	84.8	742	4	US-10-741-601-338	Sequence 338, App	204	27	81.8	178	4	US-10-190-115-24	Sequence 24, Appl1
132	28	84.8	742	4	US-10-741-601-339	Sequence 339, App	205	27	81.8	179	4	US-10-369-072-24	Sequence 24, Appl1
133	28	84.8	742	5	US-10-473-127-1382	Sequence 1282, Ap	206	27	81.8	180	4	US-10-437-963-194294	Sequence 194294,
134	28	84.8	742	5	US-10-473-127-1386	Sequence 1286, Ap	207	27	81.8	181	4	US-10-369-493-12792	Sequence 12792, A
135	28	84.8	742	5	US-10-473-127-1311	Sequence 1311, Ap	208	27	81.8	182	4	US-10-028-072-138	Sequence 138, App
136	28	84.8	742	5	US-10-473-127-1319	Sequence 1319, Ap	209	27	81.8	183	4	US-10-140-808-138	Sequence 138, App
137	28	84.8	742	5	US-10-690-880-40	Sequence 40, Appl	210	27	81.8	184	4	US-10-121-049-138	Sequence 138, App
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142	28	84.8	742	5	US-10-287-436A-445	Sequence 445, App	215	27	81.8	189	4	US-10-176-921-138	Sequence 138, App
143	28	84.8	742	5	US-10-287-436A-445	Sequence 445, App	216	27	81.8	190	4	US-10-137-865-138	Sequence 138, App
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147	28	84.8	920	5	US-10-450-763-47426	Sequence 47426, A	220	27	81.8	194	4	US-10-123-262-138	Sequence 138, App
148	28	84.8	1024	3	US-09-864-921-97	Sequence 97, Appl1	221	27	81.8	195	4	US-10-142-431-138	Sequence 138, App
149	28	84.8	1024	4	US-10-156-733-2	Sequence 2, Appl1	222	27	81.8	196	4	US-10-123-262-138	Sequence 138, App
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152	28	84.8	1024	4	US-10-766-682-37	Sequence 37, Appl	225	27	81.8	199	4	US-10-143-032-138	Sequence 138, App
153	28	84.8	1061	6	US-11-097-143-33270	Sequence 33270, A	226	27	81.8	200	4	US-10-123-108-138	Sequence 138, App
154	28	84.8	1070	4	US-10-821-09-49	Sequence 49, Appl	227	27	81.8	201	4	US-10-123-236-138	Sequence 138, App
155	28	84.8	1204	3	US-09-841-739-5	Sequence 5, Appl1	228	27	81.8	202	4	US-10-123-236-138	Sequence 138, App
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158	27	81.8	54	4	US-10-425-115-234373	Sequence 234373, A	231	27	81.8	205	4	US-10-123-262-138	Sequence 138, App
159	27	81.8	58	4	US-10-424-599-157790	Sequence 157790, A	232	27	81.8	206	4	US-10-123-262-138	Sequence 138, App
160	27	81.8	60	4	US-10-424-599-157790	Sequence 157790, A	233	27	81.8	207	4	US-10-123-262-138	Sequence 138, App
161	27	81.8	63	4	US-10-424-599-260542	Sequence 260542, A	234	27	81.8	208	4	US-10-123-262-138	Sequence 138, App
162	27	81.8	69	4	US-10-425-115-256788	Sequence 256788, A	235	27	81.8	209	4	US-10-123-262-138	Sequence 138, App
163	27	81.8	70	4	US-10-424-599-262737	Sequence 262737, A	236	27	81.8	210	4	US-10-123-262-138	Sequence 138, App
164	27	81.8	73	4	US-10-424-599-119650	Sequence 119650, A	237	27	81.8	211	4	US-10-123-262-138	Sequence 138, App
165	27	81.8	77	4	US-10-425-115-194250	Sequence 194250, A	238	27	81.8	212	4	US-10-123-262-138	Sequence 138, App
166	27	81.8	88	4	US-10-425-115-54955	Sequence 54955, A	239	27	81.8	213	4	US-10-123-262-138	Sequence 138, App
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170	27	81.8	105	4	US-10-425-115-204131	Sequence 204131, A	243	27	81.8	217	4	US-10-127-839A-138	Sequence 138, App
171	27	81.8	122	4	US-10-425-115-166562	Sequence 166562, A	244	27	81.8	218	4	US-10-127-839A-138	Sequence 138, App
172	27	81.8	123	4	US-10-425-115-366313	Sequence 366313, A	245	27	81.8	219	4	US-10-128-693A-138	Sequence 138, App
173	27	81.8	140	4	US-10-437-963-126434	Sequence 126434, A	246	27	81.8	220	4	US-10-131-813A-138	Sequence 138, App

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:04 ; Search time 6.14286 Seconds

(Without alignments)  
48.418 Million cell updates/sec

Title: US-10-067-484-4

Perfect score: 33

Sequence: 1 FXYFSRK 7

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:  
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2: /SIDBS/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /SIDBS/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
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8: /SIDBS/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	87.9	85	US-10-467-657-7040	Sequence 7040, Ap
2	87.9	85	US-10-467-657-7972	Sequence 7972, Ap
3	87.9	565	US-11-079-463-7488	Sequence 7488, Ap
4	84.8	361	US-10-995-561-612	Sequence 612, App
5	84.8	361	US-11-130-206-6	Sequence 6, App1
6	84.8	395	US-10-995-561-614	Sequence 614, App
7	84.8	425	US-10-995-561-616	Sequence 616, App
8	84.8	455	US-11-079-463-8908	Sequence 8908, Ap
9	84.8	493	US-10-995-561-611	Sequence 611, App
10	84.8	535	US-10-995-561-610	Sequence 610, App
11	84.8	691	US-10-995-561-617	Sequence 617, App
12	84.8	699	US-11-130-206-4	Sequence 4, App1
13	84.8	700	US-11-130-206-2	Sequence 2, App1
14	84.8	742	US-10-995-561-615	Sequence 615, App
15	84.8	742	US-10-995-561-618	Sequence 618, App
16	84.8	742	US-11-169-041-184	Sequence 184, App
17	84.8	742	US-11-072-175-176	Sequence 176, App
18	84.8	898	US-11-145-631-11	Sequence 11, App1
19	84.8	1024	US-11-145-631-2	Sequence 2, App1
20	84.8	1070	US-11-147-047-49	Sequence 49, App1
21	84.8	1204	US-11-145-631-5	Sequence 5, App1
22	81.8	226	US-11-087-099-8177	Sequence 8177, Ap
23	81.8	226	US-11-188-238-7554	Sequence 7554, Ap
24	81.8	232	US-11-087-099-8077	Sequence 8077, Ap
25	81.8	232	US-11-188-238-18486	Sequence 18486, A

26	81.8	447	US-11-079-463-6421	Sequence 6421, Ap
27	81.8	478	US-10-131-826A-138	Sequence 138, App
28	81.8	478	US-10-973-115B-138	Sequence 138, App
29	81.8	478	US-11-174-150-27	Sequence 27, App1
30	81.8	478	US-11-290-153-138	Sequence 138, App
31	81.8	524	US-11-024-959-378	Sequence 378, App
32	81.8	552	US-11-188-298-1024	Sequence 1024, Ap
33	81.8	572	US-11-087-099-4593	Sequence 4593, Ap
34	81.8	572	US-11-087-099-7113	Sequence 7113, Ap
35	81.8	572	US-11-188-298-15206	Sequence 15206, A
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37	81.8	579	US-11-188-298-9974	Sequence 9974, Ap
38	81.8	817	US-11-012-762-2	Sequence 2, App1
39	81.8	1770	US-11-103-357-21	Sequence 21, App1
40	81.8	1770	US-11-018-868-17	Sequence 17, App1
41	81.8	238	US-11-079-463-6309	Sequence 6309, App
42	81.8	377	US-11-087-099-10209	Sequence 10209, A
43	81.8	403	US-11-188-298-5107	Sequence 5107, Ap
44	81.8	476	US-11-087-099-10733	Sequence 10733, A
45	81.8	525	US-11-188-298-3842	Sequence 3842, Ap
46	81.8	543	US-11-072-512-3493	Sequence 3493, Ap
47	81.8	591	US-11-096-568A-33157	Sequence 33157, A
48	81.8	932	US-11-017-550-65	Sequence 65, App1
49	81.8	932	US-11-002-387-65	Sequence 65, App1
50	81.8	1092	US-10-821-234-999	Sequence 999, App
51	81.8	124	US-11-188-298-15506	Sequence 15506, A
52	81.8	226	US-11-096-568A-19476	Sequence 19476, A
53	81.8	228	US-11-096-568A-19475	Sequence 19475, A
54	81.8	240	US-11-079-463-5566	Sequence 5566, Ap
55	81.8	246	US-11-096-568A-19474	Sequence 19474, A
56	81.8	313	US-10-793-626-2500	Sequence 2500, Ap
57	81.8	365	US-11-096-568A-16949	Sequence 16949, A
58	81.8	388	US-11-079-463-6897	Sequence 6897, Ap
59	81.8	390	US-11-079-463-8590	Sequence 8590, Ap
60	81.8	455	US-11-096-568A-29406	Sequence 29406, A
61	81.8	455	US-11-096-568A-29757	Sequence 29757, A
62	81.8	458	US-11-069-642-3	Sequence 3, App1
63	81.8	458	US-11-096-568A-6564	Sequence 6564, App
64	81.8	459	US-11-096-568A-29405	Sequence 29405, A
65	81.8	462	US-11-096-568A-30639	Sequence 30639, A
66	81.8	464	US-11-096-568A-6563	Sequence 6563, Ap
67	81.8	468	US-11-079-463-8955	Sequence 8955, Ap
68	81.8	472	US-11-188-298-13633	Sequence 13633, A
69	81.8	485	US-11-096-568A-6562	Sequence 6562, Ap
70	81.8	520	US-11-096-568A-16948	Sequence 16948, A
71	81.8	612	US-11-218-020-9	Sequence 9, App1
72	81.8	662	US-11-188-298-13798	Sequence 13798, A
73	81.8	677	US-11-079-463-9704	Sequence 9704, Ap
74	81.8	703	US-11-079-463-8735	Sequence 8735, Ap
75	81.8	703	US-11-079-463-6318	Sequence 6318, Ap
76	81.8	76	US-11-079-463-8769	Sequence 8769, Ap
77	81.8	110	US-11-079-463-7365	Sequence 7365, Ap
78	81.8	120	US-11-079-463-7644	Sequence 7644, Ap
79	81.8	131	US-11-096-568A-21423	Sequence 21423, A
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83	81.8	181	US-11-079-463-8003	Sequence 8003, Ap
84	81.8	198	US-11-087-099-9365	Sequence 9365, Ap
85	81.8	209	US-10-194-487-470	Sequence 470, App
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100	24	72.7	375	7	US-11-051-267-12	Sequence 12, Appl	173	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
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106	24	72.7	392	6	US-10-873-528-442	Sequence 142, App	179	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
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117	24	72.7	535	7	US-11-096-568A-2229	Sequence 2229, Ap	190	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
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122	24	72.7	724	7	US-10-467-657-10316	Sequence 6374, Ap	195	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
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129	24	72.7	2197	7	US-11-469-679A-48	Sequence 48, Appl	202	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
130	23	69.7	13	6	US-10-469-679A-50	Sequence 50, Appl	203	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
131	23	69.7	13	6	US-10-469-679A-51	Sequence 51, Appl	204	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
132	23	69.7	13	6	US-10-469-679A-114	Sequence 114, Appl	205	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
133	23	69.7	13	6	US-10-469-679A-114	Sequence 114, Appl	206	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
134	23	69.7	15	6	US-10-469-679A-115	Sequence 115, Appl	207	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
135	23	69.7	15	6	US-10-469-679A-116	Sequence 116, Appl	208	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
136	23	69.7	19	7	US-11-129-741-3339	Sequence 8359, Ap	209	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
137	23	69.7	19	7	US-11-129-741-3339	Sequence 8359, Ap	210	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
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141	23	69.7	70	7	US-11-038-885A-3	Sequence 3, Appl	214	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
142	23	69.7	83	7	US-11-079-463-9423	Sequence 9423, Ap	215	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
143	23	69.7	99	7	US-11-207-078-19	Sequence 194, App	216	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
144	23	69.7	112	7	US-11-049-536-52	Sequence 552, App	217	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
145	23	69.7	112	7	US-11-139-318-34	Sequence 34, Appl	218	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
146	23	69.7	120	7	US-11-121-813A-4	Sequence 4, Appl	219	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
147	23	69.7	120	7	US-11-096-568A-11244	Sequence 16244, A	220	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
148	23	69.7	121	7	US-10-489-570-1926	Sequence 1926, Ap	221	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
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152	23	69.7	147	7	US-11-156-084A-148	Sequence 148, Appl	225	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
153	23	69.7	164	6	US-10-469-679A-7	Sequence 7, Appl	226	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
154	23	69.7	165	6	US-10-519-390-8	Sequence 8, Appl	227	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
155	23	69.7	165	6	US-10-469-679A-5	Sequence 5, Appl	228	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
156	23	69.7	165	6	US-10-469-679A-6	Sequence 6, Appl	229	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
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169	23	69.7	165	6	US-10-469-679A-9	Sequence 9, Appl	242	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
170	23	69.7	165	6	US-10-469-679A-9	Sequence 9, Appl	243	23	69.7	165	7	US-11-175-690-457	Sequence 457, App
171	23	69.7	165	6	US-10-469-679A-9	Sequence 9, Appl	244	23	69.7	165	7	US-11-175-690-457	Sequence 457, App

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:40:47 ; Search time 100.816 Seconds

(without alignments)  
43.582 Million cell updates/sec

Title: US-10-067-484-5

Perfect score: 43

Sequence: 1 FYATEVXDXD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	35	81.4	13	5	ABBB1974
3	34	79.1	13	5	ABBB1974
4	34	79.1	34	5	ADBS3345
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26	31	72.1	452	8	ADK65768	Adk65768 Plant ful
27	31	72.1	454	6	AAE38286	Aae38286 Rice enha
28	31	72.1	469	7	ABM89724	Abm89724 Rice abio
29	31	72.1	500	9	ADM69549	Adm69549 HIV-1 gp1
30	31	72.1	516	6	ABU52955	Abu52955 Protein e
31	31	72.1	823	6	AAU41924	Aau41924 Protonib
32	31	72.1	823	6	ABM38443	Abm38443 Protonib
33	31	72.1	961	6	ABM6081	Abm6081 Protonib
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35	31	72.1	971	6	ABM46937	Abm46937 Protonib
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38	30	69.8	44	8	ADR58152	Adr58152 Novel ant
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40	30	69.8	123	8	ADP29814	Adp29814 Human sec
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52	30	69.8	446	6	ABO27178	Abu27178 Human sig
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54	30	69.8	508	6	ADU24797	Adu24797 HIV-1 gpl
55	30	69.8	537	8	ADY08986	Ady08986 Protein e
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59	30	69.8	658	8	ADX91654	Adx91654 Plant ful
60	30	69.8	658	4	AAU65557	Aau65557 Novel pro
61	30	69.8	688	4	AAU39237	Aau39237 Human pol
62	30	69.8	688	5	ABG69494	Abg69494 Rat bait
63	30	69.8	688	5	ADG12802	Adg12802 Human GRK
64	30	69.8	688	8	ADG12804	Adg12804 Bovine GR
65	30	69.8	688	8	ADT29202	Adt29202 Human MAR
66	30	69.8	688	9	ADK05743	Adk05743 Cyclin-de
67	30	69.8	698	4	AAU41023	Aau41023 Human pol
68	30	69.8	874	8	ADP99041	Adp99041 C. albica
69	30	69.8	1027	7	ADC97048	Adc97048 E. faeciu
70	30	69.8	1072	9	ABM66373	Abm66373 M. xanthu
71	30	69.8	1371	9	ABM66825	Abm66825 M. xanthu
72	30	69.8	1516	4	AAU11435	Aau11435 C. albica
73	30	69.8	1552	8	ADBS30219	Adbs30219 Bacteri
74	30	69.8	1741	6	ABU22363	Abu22363 Protein e
75	30	69.8	2680	7	ABO61456	Abu61456 Klebsiell
76	30	69.8	2872	6	ABU22213	Abu22213 Protein e
77	29	67.4	73	3	AAU59448	Aau59448 Arabidops
78	29	67.4	74	3	AAU59447	Aau59447 Arabidops
79	29	67.4	108	4	AAU24452	Aau24452 Human sec
80	29	67.4	146	4	AAU880039	Aau880039 Coryneb
81	29	67.4	149	8	AAU55356	Aau55356 Human 5'
82	29	67.4	149	8	ADU72920	Adu72920 Non-signa
83	29	67.4	149	9	ADU73911	Adu73911 Human inc
84	29	67.4	186	4	AAU80038	Aau80038 Coryneb
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86	29	67.4	209	3	AAU24484	Aau24484 Human sec
87	29	67.4	209	3	AAU18915	Aau18915 A novel p
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97	29	67.4	209	6	ABU82940	Abu82940 Human PRO

98	29	67.4	209	6	ABU90061	Novel	hum	171	29	67.4	209	6	ABU83887	Human	sec	239	67.4	209	6	ABU808261
99	29	67.4	209	6	ABU96310	Novel	hum	172	29	67.4	209	6	ABU81972	Novel	hum	239	67.4	209	6	ABU81972
100	29	67.4	209	6	ABU96346	Novel	hum	173	29	67.4	209	6	ABU81136	Novel	hum	239	67.4	209	6	ABU81136
101	29	67.4	209	6	ABU92794	Human	sec	174	29	67.4	209	6	ABU866136	Human	sec	239	67.4	209	6	ABU866136
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103	29	67.4	209	6	ABU088871	Human	sec	176	29	67.4	209	6	ABU941153	Novel	hum	239	67.4	209	6	ABU941153
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105	29	67.4	209	6	ABU75077	Human	sec	178	29	67.4	209	6	ABU66676	Human	sec	239	67.4	209	6	ABU66676
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137	29	67.4	209	6	ABU00388	Human	sec	210	29	67.4	209	6	ABU005158	Human	PRO	239	67.4	209	6	ABU005158
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139	29	67.4	209	6	ABU01298	Human	sec	212	29	67.4	209	6	ABU005573	Human	sec	239	67.4	209	6	ABU005573
140	29	67.4	209	6	ABU02589	Human	sec	213	29	67.4	209	6	ABU88654	Human	sec	239	67.4	209	6	ABU88654
141	29	67.4	209	6	ABU02448	Human	PRO	214	29	67.4	209	6	ABU77475	Human	sec	239	67.4	209	6	ABU77475
142	29	67.4	209	6	ABU95443	Novel	hum	215	29	67.4	209	6	ABU895754	Human	sec	239	67.4	209	6	ABU895754
143	29	67.4	209	6	ABU71346	Human	PRO	216	29	67.4	209	6	ABU881356	Human	sec	239	67.4	209	6	ABU881356
144	29	67.4	209	6	ABU00785	Human	PRO	217	29	67.4	209	6	ABU881356	Human	sec	239	67.4	209	6	ABU881356
145	29	67.4	209	6	ABU70197	Human	sec	218	29	67.4	209	6	ABU001052	Human	sec	239	67.4	209	6	ABU001052
146	29	67.4	209	6	ABU65930	Human	PRO	219	29	67.4	209	6	ABU88654	Human	sec	239	67.4	209	6	ABU88654
147	29	67.4	209	6	ABU65908	Human	sec	220	29	67.4	209	6	ABU77475	Human	sec	239	67.4	209	6	ABU77475
148	29	67.4	209	6	ABU65908	Human	PRO	221	29	67.4	209	6	ABU28959	Human	sec	239	67.4	209	6	ABU28959
149	29	67.4	209	6	ABU01671	Human	PRO	222	29	67.4	209	6	ABU31104	Human	sec	239	67.4	209	6	ABU31104
150	29	67.4	209	6	ABU81471	Human	PRO	223	29	67.4	209	6	ABU76554	Novel	hum	239	67.4	209	6	ABU76554
151	29	67.4	209	6	ABU60270	Human	sec	224	29	67.4	209	6	ABU08121	Human	sec	239	67.4	209	6	ABU08121
152	29	67.4	209	6	ABU68005	Human	sec	225	29	67.4	209	6	ABU040601	Human	sec	239	67.4	209	6	ABU040601
153	29	67.4	209	6	ABU65393	Human	sec	226	29	67.4	209	6	ABU036026	Human	PRO	239	67.4	209	6	ABU036026
154	29	67.4	209	6	ABU66615	Human	sec	227	29	67.4	209	6	ABU44165	Human	PRO	239	67.4	209	6	ABU44165
155	29	67.4	209	6	ABU72027	Human	sec	228	29	67.4	209	6	ABU78222	Human	sec	239	67.4	209	6	ABU78222
156	29	67.4	209	6	ABU85507	Human	PRO	229	29	67.4	209	6	ABU24960	Human	sec	239	67.4	209	6	ABU24960
157	29	67.4	209	6	ABU88197	Human	sec	230	29	67.4	209	6	ABU00328	Human	sec	239	67.4	209	6	ABU00328
158	29	67.4	209	6	ABU88327	Human	sec	231	29	67.4	209	6	ABU90484	Human	sec	239	67.4	209	6	ABU90484
159	29	67.4	209	6	ABU95133	Novel	hum	232	29	67.4	209	6	ABU17398	Human	sec	239	67.4	209	6	ABU17398
160	29	67.4	209	6	ABU90681	Novel	hum	233	29	67.4	209	6	ABU95144	Human	sec	239	67.4	209	6	ABU95144
161	29	67.4	209	6	ABU84192	Human	sec	234	29	67.4	209	6	ABU95449	Human	sec	239	67.4	209	6	ABU95449
162	29	67.4	209	6	ABU93843	Novel	hum	235	29	67.4	209	6	ABU021687	Human	sec	239	67.4	209	6	ABU021687
163	29	67.4	209	6	ABU65088	Human	sec	236	29	67.4	209	6	ABU97951	Human	sec	239	67.4	209	6	ABU97951
164	29	67.4	209	6	ABU68920	Human	sec	237	29	67.4	209	6	ABU887739	Human	sec	239	67.4	209	6	ABU887739
165	29	67.4	209	6	ABU006736	Human	sec	238	29	67.4	209	6	ABU77780	Human	sec	239	67.4	209	6	ABU77780
166	29	67.4	209	6	ABU99281	Human	sec	239	29	67.4	209	6	ABU28010	Human	sec	239	67.4	209	6	ABU28010
167	29	67.4	209	6	ABU57165	Human	sec	240	29	67.4	209	6	ABU06291	Human	sec	239	67.4	209	6	ABU06291
168	29	67.4	209	6	ABU86117	Novel	hum	241	29	67.4	209	6	ABU003797	Human	sec	239	67.4	209	6	ABU003797
169	29	67.4	209	6	ABU82404	Novel	hum	242	29	67.4	209	6	ABU35248	Human	sec	239	67.4	209	6	ABU35248



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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:12 ; Search time 9.18367 Seconds  
(without alignments)  
104.769 Million cell updates/sec

Title: US-10-067-484-5

Perfect score: 43

Sequence: 1 FYATEVXDXD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	79.1	398	2	G95205	glycosyl transfera
2	32	74.4	357	2	B81292	hypothetical prote
3	32	74.4	510	2	B60280	bacillolysin-like
4	32	74.4	829	2	E87305	TonB-dependent rec
5	32	74.4	1186	2	S70430	hypothetical prote
6	31	72.1	63	2	E69800	hypothetical prote
7	31	72.1	210	2	E75315	probable c-type cy
8	31	72.1	212	2	C43310	stringent starvati
9	31	72.1	418	2	E65014	xanthosine permeas
10	31	72.1	428	2	T06464	protein kinase (EC
11	31	72.1	433	2	A55333	monodehydroascorba
12	31	72.1	454	2	T03780	probable integral
13	31	72.1	710	2	T26742	hypothetical prote
14	31	72.1	1079	2	T18356	membrane protein p
15	31	72.1	1207	2	B88789	protein ZK1251.9
16	31	72.1	1211	2	T23210	hypothetical prote
17	30	69.8	114	2	S77061	transposase sl1066
18	30	69.8	176	2	AB0777	probable lipoprote
19	30	69.8	229	2	D90002	hypothetical prote
20	30	69.8	257	2	T34089	hypothetical prote
21	30	69.8	259	2	S76643	transposase slr051
22	30	69.8	261	2	S75081	transposase slr026
23	30	69.8	261	2	S77171	transposase sl1171
24	30	69.8	261	2	S77351	transposase sl1171
25	30	69.8	261	2	S76309	transposase slr035
26	30	69.8	305	2	C69465	diironoxenase redu
27	30	69.8	314	1	WMBB84	ribonucleoside-dip
28	30	69.8	314	2	H88991	protein K0899.1
29	30	69.8	433	2	T06407	monodehydroascorba

30	30	69.8	434	2	JU0182	monodehydroascorba
31	30	69.8	571	2	AG0144	D-lactate dehydrog
32	30	69.8	584	2	S06318	endoplasmic reticu
33	30	69.8	638	1	ISM58R	protein disulfide-
34	30	69.8	643	1	S32476	protein disulfide-
35	30	69.8	688	1	UC1469	beta-adrenergic-re
36	30	69.8	688	1	A39336	beta-adrenergic-re
37	30	69.8	882	1	E96931	hypothetical prote
38	30	69.8	1010	2	T36383	probable large ATP
39	29	67.4	115	2	H72643	hypothetical prote
40	29	67.4	230	2	B86824	two-component gyt
41	29	67.4	256	2	A11204	molybdate ABC tran
42	29	67.4	326	2	T09259	cathepsin L-like p
43	29	67.4	326	2	E84812	hypothetical prote
44	29	67.4	347	2	S67159	probable membrane
45	29	67.4	388	2	D84992	hypothetical prote
46	29	67.4	390	2	C90288	hypothetical prote
47	29	67.4	392	2	G82746	hypothetical prote
48	29	67.4	395	2	C83788	galactokinase (imp
49	29	67.4	400	2	G89772	hypothetical prote
50	29	67.4	462	2	T26401	hypothetical prote
51	29	67.4	470	2	G85911	hypothetical prote
52	29	67.4	543	2	F91067	hypothetical prote
53	29	67.4	690	2	T01183	hypothetical prote
54	29	67.4	788	2	AF0122	probable membrane
55	29	67.4	877	2	S58824	rep-1 protein, for
56	29	67.4	929	2	A32495	hypothetical prote
57	29	67.4	1081	2	T00330	DNA mismatch repai
58	29	67.4	1126	2	JC4019	immunoglobulin Al
59	29	67.4	2004	2	F95133	hypothetical prote
60	28	65.1	139	2	T29394	hypothetical prote
61	28	65.1	161	2	T22196	hypothetical prote
62	28	65.1	161	2	T20676	hypothetical prote
63	28	65.1	201	2	G59096	hypothetical prote
64	28	65.1	214	2	S74663	peptide methionine
65	28	65.1	234	2	S24365	holocytochrome-c
66	28	65.1	220	2	F83697	ABC transporter (A
67	28	65.1	262	2	T17442	YbtF protein - Yer
68	28	65.1	262	2	E90156	undecaprenyl diph
69	28	65.1	267	2	AH0232	yersiniabactin bio
70	28	65.1	267	2	T30344	YlpA protein - Yer
71	28	65.1	267	2	T47050	hypothetical prote
72	28	65.1	273	2	T31506	positive transcrip
73	28	65.1	286	2	G86770	GDP-D-mannose dehy
74	28	65.1	309	2	C84167	exogastrolu-induci
75	28	65.1	325	2	A40084	hypothetical prote
76	28	65.1	327	2	C97663	conserved hypochet
77	28	65.1	327	2	AF2887	UDP-glucose 4-epim
78	28	65.1	339	2	B95187	UDPglucose 4-epime
79	28	65.1	339	2	C98054	mitogen-activated
80	28	65.1	369	2	S56638	mitogen-activated
81	28	65.1	371	2	T14915	mitogen-activated
82	28	65.1	375	2	T03971	probable sugar iso
83	28	65.1	389	2	B90431	sulfolipid biosynt
84	28	65.1	389	2	E90431	p54-gamma stress-a
85	28	65.1	411	2	S43970	p54-beta stress-ac
86	28	65.1	426	2	S43969	hypothetical prote
87	28	65.1	431	2	T29716	2,2-dialkylglycine
88	28	65.1	431	2	A35173	aminotransferase,
89	28	65.1	435	2	AH3196	hypothetical prote
90	28	65.1	436	2	C89926	phosphoglycerate d
91	28	65.1	436	2	B95199	GTP-binding protei
92	28	65.1	436	2	H98065	hypothetical prote
93	28	65.1	436	2	C86719	hypothetical prote
94	28	65.1	437	2	T24953	monodehydroascorba
95	28	65.1	437	2	T48390	hypothetical prote
96	28	65.1	458	2	S76009	chromosome replica
97	28	65.1	458	2	A11269	protein kinase JNK
98	28	65.1	464	2	S71104	beta-actin-like
99	28	65.1	510	2	A60280	zinc metalloprotei
100	28	65.1	510	2	AD1100	isomerase fucI (EC
101	28	65.1	604	2	F64081	probable serine/th
102	28	65.1	607	2	S62556	

103	28	65.1	621	2	JC7892	acyl-CoA dehydrog
104	28	65.1	634	2	H64508	hypothetical prote
105	28	65.1	652	2	T02001	hypothetical prote
106	28	65.1	667	2	T01999	hypothetical prote
107	28	65.1	687	2	A41905	ferric vibriobacti
108	28	65.1	715	2	D84480	Mutator-like trans
109	28	65.1	725	2	T20674	hypothetical prote
110	28	65.1	726	2	T40373	probable thiorodox
111	28	65.1	760	2	S64023	AlrK protein - yea
112	28	65.1	760	2	T02808	conserved hypotet
113	28	65.1	962	2	G86479	F1AD7.6 protein -
114	28	65.1	969	2	T03657	NAD ADP-riboseyltra
115	28	65.1	1026	2	A49750	beta-galactosidase
116	28	65.1	1162	2	A12843	carbamoylphosphate
117	28	65.1	1186	2	B97621	hypothetical prote
118	28	65.1	1307	2	T35944	probable beta-gala
119	28	65.1	2077	1	MZBR24	240K tegument pro
120	28	65.1	2077	2	T44178	large tegument pro
121	28	65.1	2077	2	T43991	legument protein -
122	28	65.1	2078	2	T09326	ycwB protein - Bac
123	27	62.8	87	2	S39696	hypothetical prote
124	27	62.8	88	2	D70010	ferredoxin [import
125	27	62.8	98	2	A98322	conserved hypotet
126	27	62.8	107	2	T46583	protein-tyrosine k
127	27	62.8	125	2	B87297	hypothetical cytos
128	27	62.8	127	2	B49300	hypothetical prote
129	27	62.8	143	2	B39061	hypothetical prote
130	27	62.8	149	2	AF3343	conserved hypotet
131	27	62.8	154	2	AG1162	hypothetical prote
132	27	62.8	160	2	A39061	protein-tyrosine k
133	27	62.8	161	2	AC0439	conserved hypotet
134	27	62.8	165	2	D64648	hypothetical prote
135	27	62.8	167	2	B71939	hypothetical prote
136	27	62.8	172	2	B64978	hypothetical prote
137	27	62.8	172	2	D85438	hypothetical prote
138	27	62.8	172	2	A90993	conserved hypotet
139	27	62.8	176	2	D90167	elongsat peptidase (
140	27	62.8	182	2	F83778	elongsat factor
141	27	62.8	185	2	D86711	elongsat factor
142	27	62.8	185	2	D95050	elongsat factor
143	27	62.8	186	2	H97920	probable phosphat
144	27	62.8	190	2	T39622	probable phosphat
145	27	62.8	208	2	AG0635	hypothetical prote
146	27	62.8	219	2	S67935	conserved hypotet
147	27	62.8	247	2	C83579	probable phosphos
148	27	62.8	255	2	T24364	hypothetical prote
149	27	62.8	260	2	C95380	conserved hypotet
150	27	62.8	268	2	F71712	proliporotein dta
151	27	62.8	274	2	T18768	hypothetical prote
152	27	62.8	285	1	J00851	site-specific DNA-
153	27	62.8	285	2	AB0926	menaquinone biosyn
154	27	62.8	285	2	T31325	hypothetical 32.1k
155	27	62.8	292	2	TJ4099	anexin IX - fruit
156	27	62.8	292	2	LJMP93	signal-transducin
157	27	62.8	296	1	LS9352	protein T05A8.7 [i
158	27	62.8	323	2	AB8082	probable GTP-bind
159	27	62.8	353	2	S75088	zinc finger protei
160	27	62.8	363	2	T38945	succlnvl-diaminop
161	27	62.8	372	2	F64048	probable replicat
162	27	62.8	387	2	A41661	voltage-gated pota
163	27	62.8	393	2	TJ3547	adenosylmethione
164	27	62.8	400	2	S09636	pyrB protein - Bac
165	27	62.8	401	2	T02378	hypothetical prote
166	27	62.8	402	2	C83377	glycolate oxidase
167	27	62.8	408	2	AB8327	hypothetical prote
168	27	62.8	416	2	DE9340	folylpolyglutamate
169	27	62.8	423	2	B67968	protein kinase JNK
170	27	62.8	427	2	S71097	protein kinase JNK
171	27	62.8	427	2	AB4638	pmbA protein [impo
172	27	62.8	430	2	H71172	hypothetical prote
173	27	62.8	431	2		
174	27	62.8				
175	27	62.8				
176	176	62.8	446	2	F71069	hypothetical prote
177	177	62.8	449	2	A99286	conserved hypotet
178	178	62.8	459	2	B84933	UDP-N-acetylglucos
179	179	62.8	463	2	B72500	probable g3271-ERN
180	180	62.8	471	2	F71618	adenylsuccinate 1
181	181	62.8	488	2	T48447	3-phosphoglycerate
182	182	62.8	488	2	B83786	glyceraldehyde 3-ph
183	183	62.8	497	2	H86815	hypothetical prote
184	184	62.8	506	2	T51702	amido-phosphoryl
185	185	62.8	516	2	UB0134	metan CtpA [m1-coyl
186	186	62.8	527	2	T25126	serine CtpA [m1-coyl
187	187	62.8	551	2	T11629	58k antilegal - sick
188	188	62.8	555	2	B41492	hypothetical prote
189	189	62.8	559	2	AB1153	hypothetical prote
190	190	62.8	559	2	AC1512	hypothetical prote
191	191	62.8	564	2	H70804	hypothetical prote
192	192	62.8	576	2	T25375	hypothetical prote
193	193	62.8	614	2	T19539	hypothetical prote
194	194	62.8	627	2	T19542	hypothetical prote
195	195	62.8	642	2	G64605	iron (III) transport
196	196	62.8	642	2	D71909	ferrous iron trans
197	197	62.8	642	2	T45904	protein kinase-lik
198	198	62.8	642	2	A4362	protein kinase-lik
199	199	62.8	658	2	A35447	carbamate O-palmit
200	200	62.8	658	2	G84663	hypothetical prote
201	201	62.8	676	2	S22258	probable protein k
202	202	62.8	726	2	T26096	hypothetical prote
203	203	62.8	727	2	T26096	hypothetical prote
204	204	62.8	730	2	A13480	penicillin-binding
205	205	62.8	734	2	S44617	USO33.11 protein
206	206	62.8	749	2	T46782	lanosereol synthas
207	207	62.8	754	2	AC2807	Ompa family protei
208	208	62.8	754	2	B97586	hypothetical prote
209	209	62.8	760	2	T01441	hypothetical prote
210	210	62.8	778	2	H96649	protein r240.14 [x
211	211	62.8	791	2	C97106	radi-related DNA h
212	212	62.8	799	2	T48889	serine/threonine p
213	213	62.8	801	2	S50660	hypothetical prote
214	214	62.8	802	2	AF1227	phenylalanyl-tRNA
215	215	62.8	804	2	AB1580	phenylalanyl-tRNA
216	216	62.8	826	1	A31822	DNA topoisomerase
217	217	62.8	834	2	T28250	Villin - chicken
218	218	62.8	882	2	AG1671	ORF MS7083 probab
219	219	62.8	882	2	H84506	probable peptidogl
220	220	62.8	893	2	S63378	probable retroelem
221	221	62.8	900	2	D97351	hypothetical prote
222	222	62.8	903	2	AG1299	senior protein kdp
223	223	62.8	932	2	A39931	probable peptidogl
224	224	62.8	993	2	A36873	protein-tyrosine k
225	225	62.8	995	2	A11497	Hadr type IC reacr
226	226	62.8	1000	2	S18827	F13 protein - mou
227	227	62.8	1048	2	H64459	hypothetical prote
228	228	62.8	1111	2	T09941	126k pathogenicit
229	229	62.8	1112	2	D82276	probable inner mem
230	230	62.8	1120	2	B83498	conserved hypotet
231	231	62.8	1123	2	T51517	telomerase reverse
232	232	62.8	1153	2	T31080	nitric-oxide synth
233	233	62.8	1155	2	T39040	hypothetical prote
234	234	62.8	1162	2	AD3317	carbamoyl-phosphat
235	235	62.8	1186	2	T19334	hypothetical prote
236	236	62.8	1388	2	T38720	chromodomain helic
237	237	62.8	1418	2	T15232	hypothetical prote
238	238	62.8	1518	2	T28880	hypothetical prote
239	239	62.8	2052	2	T18290	FYVE finger-contai
240	240	62.8	2180	2	A46182	polyprotein - echo
241	241	62.8	2352	2	C83329	probable non-ribos
242	242	60.5	29	2	F83870	hypothetical prote
243	243	60.5	74	2	F70526	hypothetical prote
244	244	60.5	82	1	VCBPIK	coat protein B pre
245	245	60.5	93	2	S75008	transposase sbl192
246	246	60.5	101	2	S13701	ig kappa chain V r
247	247	60.5	102	2	D84397	hypothetical prote
248	248	60.5	103	2	S13703	ig kappa chain V r

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:05 ; Search time 54.4898 Seconds  
(without alignments)  
129.479 Million cell updates/sec

Title: US-10-067-484-5  
Perfect score: 43  
Sequence: 1 FVATEVXDND 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Uniprot 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	79.1	233	2	089R8 BRAVA
2	34	79.1	246	2	040106 SHIV1
3	34	79.1	346	1	FEN_PYRAB
4	34	79.1	398	2	097P77 STRPN
5	34	79.1	449	2	088M47 LACPL
6	34	79.1	955	2	07P081 ANOGA
7	33	76.7	108	2	09J009 SHIV1
8	33	76.7	190	2	04XH19 PLACH
9	33	76.7	361	2	04Y0W3 PLACH
10	33	76.7	410	2	08ZXK3 PYRAB
11	33	76.7	436	2	08A9A2 BACTN
12	32	74.4	241	2	07XIP6 PLACT
13	32	74.4	319	2	073P18 TREDE
14	32	74.4	357	2	09PMK1 CAMUE
15	32	74.4	510	1	PRO2_LISMO
16	32	74.4	510	2	06E9N9 LISMO
17	32	74.4	510	2	06E9A9 LISMO
18	32	74.4	510	2	06EAC2 LISMO
19	32	74.4	510	2	06EAT1 LISMO
20	32	74.4	510	2	06EAG9 LISMO
21	32	74.4	510	2	06EAB8 LISMO
22	32	74.4	510	2	0724L0 LISMF
23	32	74.4	512	1	NRAM4 ARATH
24	32	74.4	570	2	04N3C1 THEPA
25	32	74.4	583	2	04UAL9 THEAN
26	32	74.4	594	2	08KUV5 GEOKA
27	32	74.4	624	2	0974Z9 DROME
28	32	74.4	788	2	04MMK4 BACCE
29	32	74.4	809	2	072LY1 LEPC
30	32	74.4	809	2	08EYF2 LEPC
31	32	74.4	829	2	09AAV8 CAUCR

32	32	74.4	854	2	09S3P8 STRPY	09S3P8 streptococ
33	32	74.4	862	2	09RP22 STRPY	09RP22 streptococ
34	32	74.4	865	2	09S4J9 STRPY	09S4J9 streptococ
35	32	74.4	872	2	09S4J3 STRPY	09S4J3 streptococ
36	32	74.4	1027	2	06A708 PROAC	06A708 propionibac
37	32	74.4	2504	2	04OP93 LEIMA	04OP93 leishmania
38	31	72.1	34	2	07SP88 SHIV1	07SP88 human immun
39	31	72.1	34	2	07SP71 SHIV1	07SP71 human immun
40	31	72.1	35	2	097632 SHIV1	097632 human immun
41	31	72.1	63	1	YFHD BACSV	031572 bacillus su
42	31	72.1	82	2	056682 SHIV1	056682 human immun
43	31	72.1	91	2	086879 SHIV1	086879 human immun
44	31	72.1	94	2	05P0V6 SHIV1	05P0V6 human immun
45	31	72.1	95	2	074529 SHIV1	074529 human immun
46	31	72.1	102	2	090RU5 SHIV1	090RU5 human immun
47	31	72.1	106	2	037956 SHIV1	037956 human immun
48	31	72.1	119	2	07ZKW7 SHIV1	07ZKW7 human immun
49	31	72.1	114	2	07ZB10 SHIV1	07ZB10 human immun
50	31	72.1	137	2	05DEP4 SCHUA	05DEP4 schistosoma
51	31	72.1	166	1	MDARF CUCSA	097869 deinococcus
52	31	72.1	210	2	09RSM9 DEIRA	031784 haemophilus
53	31	72.1	212	1	SSPA HBEO	050342 haemophilus
54	31	72.1	212	2	050342 HAEN	050342 human immun
55	31	72.1	215	2	088084 SHIV1	088084 human immun
56	31	72.1	225	2	04H8G4_9DEIO	04H8G4 deinococcus
57	31	72.1	236	2	04YUX0 PLABE	04YUX0 plasmodium
58	31	72.1	242	2	05XWE3 PEA	05XWE3 plasmodium
59	31	72.1	250	2	05AP52 CANML	05AP52 candida alb
60	31	72.1	260	2	07MS87 WOLSU	07MS87 wolinstella s
61	31	72.1	342	2	04FLU4_9RICK	04FLU4 candidatus
62	31	72.1	349	2	06NDF7 RHOPA	06NDF7 rhodopsendo
63	31	72.1	364	2	09MQ24 SHIV1	09MQ24 human immun
64	31	72.1	381	2	07VZE2 BORPE	07VZE2 bordetella
65	31	72.1	381	2	07W611 BORPA	07W611 bordetella
66	31	72.1	381	2	07WCV2 BORER	07WCV2 bordetella
67	31	72.1	408	2	082SX0 STRWM	082SX0 streptomyces
68	31	72.1	413	2	030626 ECOLI	030626 escherichia
69	31	72.1	418	1	XAPB ECOLI	045562 escherichia
70	31	72.1	418	2	08FFC7 ECOL6	08FFC7 escherichia
71	31	72.1	428	2	07DMT0 PEA	07DMT0 plasmodium
72	31	72.1	433	1	MDAR_PEA	040977 plasmodium
73	31	72.1	433	2	066PF9_PEA	066PF9 plasmodium
74	31	72.1	464	2	024209 ORVSA	024209 oryza sativ
75	31	72.1	491	2	04MFX2 BACE	04MFX2 bacillus ce
76	31	72.1	494	2	0516B8 LYCES	0516B8 lycopersico
77	31	72.1	500	2	041993 GIBRE	041993 gibberella
78	31	72.1	528	2	06XDM2_PHTN	06XDM2 phytophthor
79	31	72.1	608	2	04WD04 ASPPU	04WD04 aspergillus
80	31	72.1	612	2	05LFP9 BACFN	05LFP9 bacteroides
81	31	72.1	612	2	04UW02 BACFN	04UW02 bacteroides
82	31	72.1	657	2	04UGC0 THEAN	04UGC0 theileria a
83	31	72.1	680	2	04MGV2 BACE	04MGV2 bacillus ce
84	31	72.1	698	2	07MAP6 WOLSU	07MAP6 wolinstella s
85	31	72.1	710	2	09XX10 CAEBL	09XX10 caenorhabdi
86	31	72.1	713	2	060Y97 CABER	060Y97 caenorhabdi
87	31	72.1	721	2	06J2G4 PSETH	06J2G4 pseudomonas
88	31	72.1	727	2	05UXO2 HALMA	05UXO2 haloarcula
89	31	72.1	807	2	098SD7 RHIO	098SD7 rhizobium 1
90	31	72.1	929	2	06AB64_PROAC	06AB64 propionibac
91	31	72.1	963	2	08H935 VITCA	08H935 viticia faba
92	31	72.1	971	2	06CG17 YARLI	06CG17 yarrowia li
93	31	72.1	1008	2	06BVE3 DEBNA	06BVE3 debaryomyces
94	31	72.1	1041	2	04IS31 GIBRE	04IS31 gibberella
95	31	72.1	1079	2	049555 MYCNO	049555 mycoplasma
96	31	72.1	1701	2	021106 CAEBL	021106 caenorhabdi
97	31	69.8	34	2	09OR28 SHIV1	09OR28 human immun
98	30	69.8	57	2	09OD59 SHIV1	09OD59 human immun
99	30	69.8	59	2	06F7L6 ACIND	06F7L6 acinetobact
100	30	69.8	61	2	09YZ87 SHIV1	09YZ87 human immun
101	30	69.8	61	2	09YZ88 SHIV1	09YZ88 human immun
102	30	69.8	61	2	09YZ89 SHIV1	09YZ89 human immun
103	30	69.8	69	2	05UG02 SHIV1	05UG02 human immun
104	30	69.8	69	2	05UG03 SHIV1	05UG03 human immun

105	30	69.8	69	2	OSUG9_9H1V1	OSUG9	human	immun	178	30	69.8	129	2	Q89CN6_BRAVA	Q89CN6	bradyrhizob
106	30	69.8	69	2	OSUCM4_9H1V1	OSUCM4	human	immun	179	30	69.8	139	2	Q75346_9H1V1	Q75346	human immun
107	30	69.8	69	2	OSUCM7_9H1V1	OSUCM7	human	immun	180	30	69.8	147	2	Q533V2_URSAR	Q533V2	ureus arcto
108	30	69.8	74	2	Q90T06_9H1V1	Q90T06	human	immun	181	30	69.8	147	2	Q533V4_AILME	Q533V4	ailuropoda
109	30	69.8	76	2	Q57M13_SALCH	Q57M13	salmonella		182	30	69.8	147	2	Q533V5_PROLO	Q533V5	procyon lot
110	30	69.8	86	2	P89405_9H1V1	P89405	human	immun	183	30	69.8	147	2	Q533V6_POTFL	Q533V6	potos flavu
111	30	69.8	86	2	Q90AC4_9H1V1	Q90AC4	human	immun	184	30	69.8	147	2	Q533V7_ERIBA	Q533V7	erignathus
112	30	69.8	86	2	Q9DX07_9H1V1	Q9DX07	human	immun	185	30	69.8	147	2	Q533V8_ZALCA	Q533V8	zalophus ca
113	30	69.8	88	2	Q10S29_9H1V1	Q10S29	human	immun	186	30	69.8	147	2	Q533Y9_CALUR	Q533Y9	callophus
114	30	69.8	88	2	Q79223_9H1V1	Q79223	human	immun	187	30	69.8	147	2	Q533Z0_CALUR	Q533Z0	callophus
115	30	69.8	92	2	Q75328_9H1V1	Q75328	human	immun	188	30	69.8	147	2	Q533Z1_9CARN	Q533Z1	odobenus ro
116	30	69.8	93	2	Q97201_9H1V1	Q97201	human	immun	189	30	69.8	147	2	Q533Z2_9CARN	Q533Z2	epilogaie p
117	30	69.8	93	2	Q97195_9H1V1	Q97195	human	immun	190	30	69.8	147	2	Q533Z3_MUSFR	Q533Z3	mephitis me
118	30	69.8	93	2	Q97202_9H1V1	Q97202	human	immun	191	30	69.8	147	2	Q533Z4_MUSFR	Q533Z4	lontea cana
119	30	69.8	94	2	Q80035_9H1V1	Q80035	human	immun	192	30	69.8	147	2	Q533Z5_LONCN	Q533Z5	muscivora
120	30	69.8	94	2	Q80037_9H1V1	Q80037	human	immun	193	30	69.8	147	2	Q533Z6_ENHIL	Q533Z6	entheda lut
121	30	69.8	94	2	Q80038_9H1V1	Q80038	human	immun	194	30	69.8	147	2	Q533Z7_9CARN	Q533Z7	conepatus m
122	30	69.8	94	2	Q80039_9H1V1	Q80039	human	immun	195	30	69.8	147	2	Q533Z8_VDLUV	Q533Z8	vulpes vulp
123	30	69.8	94	2	Q80040_9H1V1	Q80040	human	immun	196	30	69.8	147	2	Q533Z9_CANRF	Q533Z9	canis rufus
124	30	69.8	94	2	Q80041_9H1V1	Q80041	human	immun	197	30	69.8	147	2	Q534A0_CANPA	Q534A0	canis famil
125	30	69.8	94	2	Q80042_9H1V1	Q80042	human	immun	198	30	69.8	147	2	Q534A1_AILFU	Q534A1	ailurus ful
126	30	69.8	94	2	Q80043_9H1V1	Q80043	human	immun	199	30	69.8	150	2	Q534A2_SALPA	Q534A2	salmonella
127	30	69.8	94	2	Q80044_9H1V1	Q80044	human	immun	200	30	69.8	176	2	Q825C2_SALTI	Q825C2	salmonella
128	30	69.8	94	2	Q80045_9H1V1	Q80045	human	immun	201	30	69.8	176	2	Q825C2_SALTI	Q825C2	salmonella
129	30	69.8	94	2	Q80046_9H1V1	Q80046	human	immun	202	30	69.8	194	2	Q681D9_9H1V1	Q681D9	human immun
130	30	69.8	94	2	Q80047_9H1V1	Q80047	human	immun	203	30	69.8	198	2	Q534J1_9H1V1	Q534J1	human immun
131	30	69.8	94	2	Q80048_9H1V1	Q80048	human	immun	204	30	69.8	201	2	Q8A6M3_9H1V1	Q8A6M3	human immun
132	30	69.8	94	2	Q80049_9H1V1	Q80049	human	immun	205	30	69.8	214	2	Q4P474_USRMA	Q4P474	usellago ma
133	30	69.8	94	2	Q80050_9H1V1	Q80050	human	immun	206	30	69.8	220	2	Q7ZMF5_9H1V1	Q7ZMF5	human immun
134	30	69.8	94	2	Q80051_9H1V1	Q80051	human	immun	207	30	69.8	223	2	Q8AGD0_9H1V1	Q8AGD0	human immun
135	30	69.8	94	2	Q80052_9H1V1	Q80052	human	immun	208	30	69.8	228	2	Q40101_9H1V1	Q40101	human immun
136	30	69.8	94	2	Q80053_9H1V1	Q80053	human	immun	209	30	69.8	229	2	Q6G7L6_STRA6	Q6G7L6	staphylococ
137	30	69.8	94	2	Q80054_9H1V1	Q80054	human	immun	210	30	69.8	229	2	Q6G7L6_STRA6	Q6G7L6	staphylococ
138	30	69.8	94	2	Q80055_9H1V1	Q80055	human	immun	211	30	69.8	229	2	Q5HEA5_STRA6	Q5HEA5	staphylococ
139	30	69.8	94	2	Q80056_9H1V1	Q80056	human	immun	212	30	69.8	229	2	Q7ACB8_STRA6	Q7ACB8	staphylococ
140	30	69.8	94	2	Q80057_9H1V1	Q80057	human	immun	213	30	69.8	229	2	Q7ACB8_STRA6	Q7ACB8	staphylococ
141	30	69.8	94	2	Q80058_9H1V1	Q80058	human	immun	214	30	69.8	229	2	Q7ACB8_STRA6	Q7ACB8	staphylococ
142	30	69.8	95	2	Q74521_9H1V1	Q74521	human	immun	215	30	69.8	246	2	Q40114_9H1V1	Q40114	human immun
143	30	69.8	95	2	Q74522_9H1V1	Q74522	human	immun	216	30	69.8	246	2	Q40094_9H1V1	Q40094	human immun
144	30	69.8	95	2	Q74523_9H1V1	Q74523	human	immun	217	30	69.8	246	2	Q40102_9H1V1	Q40102	human immun
145	30	69.8	95	2	Q74524_9H1V1	Q74524	human	immun	218	30	69.8	246	2	Q40103_9H1V1	Q40103	human immun
146	30	69.8	95	2	Q74525_9H1V1	Q74525	human	immun	219	30	69.8	246	2	Q40104_9H1V1	Q40104	human immun
147	30	69.8	95	2	Q74526_9H1V1	Q74526	human	immun	220	30	69.8	246	2	Q40105_9H1V1	Q40105	human immun
148	30	69.8	95	2	Q74527_9H1V1	Q74527	human	immun	221	30	69.8	246	2	Q40106_9H1V1	Q40106	human immun
149	30	69.8	95	2	Q74528_9H1V1	Q74528	human	immun	222	30	69.8	246	2	Q40107_9H1V1	Q40107	human immun
150	30	69.8	95	2	Q74529_9H1V1	Q74529	human	immun	223	30	69.8	246	2	Q40108_9H1V1	Q40108	human immun
151	30	69.8	95	2	Q74530_9H1V1	Q74530	human	immun	224	30	69.8	246	2	Q40109_9H1V1	Q40109	human immun
152	30	69.8	95	2	Q74531_9H1V1	Q74531	human	immun	225	30	69.8	246	2	Q40110_9H1V1	Q40110	human immun
153	30	69.8	95	2	Q74532_9H1V1	Q74532	human	immun	226	30	69.8	246	2	Q40111_9H1V1	Q40111	human immun
154	30	69.8	95	2	Q74533_9H1V1	Q74533	human	immun	227	30	69.8	246	2	Q40112_9H1V1	Q40112	human immun
155	30	69.8	95	2	Q74534_9H1V1	Q74534	human	immun	228	30	69.8	246	2	Q40113_9H1V1	Q40113	human immun
156	30	69.8	95	2	Q74535_9H1V1	Q74535	human	immun	229	30	69.8	246	2	Q40114_9H1V1	Q40114	human immun
157	30	69.8	95	2	Q74536_9H1V1	Q74536	human	immun	230	30	69.8	246	2	Q40115_9H1V1	Q40115	human immun
158	30	69.8	95	2	Q74537_9H1V1	Q74537	human	immun	231	30	69.8	246	2	Q40116_9H1V1	Q40116	human immun
159	30	69.8	95	2	Q74538_9H1V1	Q74538	human	immun	232	30	69.8	246	2	Q40117_9H1V1	Q40117	human immun
160	30	69.8	95	2	Q74539_9H1V1	Q74539	human	immun	233	30	69.8	246	2	Q40118_9H1V1	Q40118	human immun
161	30	69.8	95	2	Q74540_9H1V1	Q74540	human	immun	234	30	69.8	246	2	Q40119_9H1V1	Q40119	human immun
162	30	69.8	95	2	Q74541_9H1V1	Q74541	human	immun	235	30	69.8	246	2	Q40120_9H1V1	Q40120	human immun
163	30	69.8	95	2	Q74542_9H1V1	Q74542	human	immun	236	30	69.8	246	2	Q40121_9H1V1	Q40121	human immun
164	30	69.8	95	2	Q74543_9H1V1	Q74543	human	immun	237	30	69.8	246	2	Q40122_9H1V1	Q40122	human immun
165	30	69.8	95	2	Q74544_9H1V1	Q74544	human	immun	238	30	69.8	246	2	Q40123_9H1V1	Q40123	human immun
166	30	69.8	95	2	Q74545_9H1V1	Q74545	human	immun	239	30	69.8	246	2	Q40124_9H1V1	Q40124	human immun
167	30	69.8	95	2	Q74546_9H1V1	Q74546	human	immun	240	30	69.8	246	2	Q40125_9H1V1	Q40125	human immun
168	30	69.8	95	2	Q74547_9H1V1	Q74547	human	immun	241	30	69.8	246	2	Q40126_9H1V1	Q40126	human immun
169	30	69.8	95	2	Q74548_9H1V1	Q74548	human	immun	242	30	69.8	246	2	Q40127_9H1V1	Q40127	human immun
170	30	69.8	95	2	Q74549_9H1V1	Q74549	human	immun	243	30	69.8	246	2	Q40128_9H1V1	Q40128	human immun
171	30	69.8	95	2	Q74550_9H1V1	Q74550	human	immun	244	30	69.8	246	2	Q40129_9H1V1	Q40129	human immun
172	30	69.8	95	2	Q74551_9H1V1	Q74551	human	immun	245	30	69.8	246	2	Q40130_9H1V1	Q40130	human immun
173	30	69.8	95	2	Q74552_9H1V1	Q74552	human	immun	246	30	69.8	246	2	Q40131_9H1V1	Q40131	human immun
174	30	69.8	95	2	Q74553_9H1V1	Q74553	human	immun	247	30	69.8	246	2	Q40132_9H1V1	Q40132	human immun
175	30	69.8	95	2	Q74554_9H1V1	Q74554	human	immun	248	30	69.8	246	2	Q40133_9H1V1	Q40133	human immun
176	30	69.8	95	2	Q74555_9H1V1	Q74555	human	immun	249	30	69.8	246	2	Q40134_9H1V1	Q40134	human immun
177	30	69.8	95	2	Q74556_9H1V1	Q74556	human	immun	250	30	69.8	246	2	Q40135_9H1V1	Q40135	human immun

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:41:21, Search time 19.3878 Seconds  
(without alignments)  
42.643 Million cell updates/sec

Title: US-10-067-484-5  
Perfect score: 43  
Sequence: 1 FVATEVXDKD 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database: Issued Patents AA:\*

- 1: /cgm2\_6/ptodata/1/iaa/5 COMB.pep:\*
- 2: /cgm2\_6/ptodata/1/iaa/6 COMB.pep:\*
- 3: /cgm2\_6/ptodata/1/iaa/H\_COMB.pep:\*
- 4: /cgm2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 5: /cgm2\_6/ptodata/1/iaa/RB\_COMB.pep:\*
- 6: /cgm2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	79.1	346	2	US-09-940-244-379 Sequence 379, App
2	34	79.1	398	2	US-09-769-787-61 Sequence 61, Appl
3	31	72.1	243	2	US-09-489-039A-8468 Sequence 8468, Ap
4	31	72.1	270	2	US-09-248-786A-14475 Sequence 14475, A
5	30	69.8	162	2	US-09-765-815-14 Sequence 14, Appl
6	30	69.8	433	1	US-08-417-492-2 Sequence 2, Appl
7	30	69.8	439	2	US-09-489-039A-8498 Sequence 8498, Ap
8	30	69.8	638	1	US-08-557-122A-38 Sequence 38, Appl
9	30	69.8	638	2	US-09-262-666-38 Sequence 38, Appl
10	30	69.8	698	2	US-09-949-016-10644 Sequence 10644, A
11	30	69.8	703	2	US-09-248-786A-14529 Sequence 14529, A
12	30	69.8	1027	2	US-09-107-532A-6675 Sequence 6675, Ap
13	30	69.8	1072	2	US-09-902-540-15572 Sequence 15572, A
14	30	69.8	1371	2	US-09-902-540-16024 Sequence 16024, A
15	30	69.8	2680	2	US-09-489-039A-7973 Sequence 7973, Ap
16	29	67.4	149	2	US-09-270-767-40126 Sequence 40126, A
17	29	67.4	149	2	US-09-270-767-40126 Sequence 40126, A
18	29	67.4	149	2	US-09-471-276-1517 Sequence 1517, Ap
19	29	67.4	347	2	US-09-538-092-753 Sequence 753, App
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23	29	67.4	877	2	US-09-771-161A-179 Sequence 179, App
24	28	65.1	108	2	US-09-909-650B-27 Sequence 27, Appl
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151	27	62.8	844	2	US-09-866-020A-29	Sequence 29, Appl1	224	27	62.8	34	2	US-09-430-323-138	Sequence 138, App
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153	27	62.8	871	2	US-09-177-650-12	Sequence 2, Appl1	226	27	62.8	34	2	US-09-721-456-256	Sequence 256, App
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158	27	62.8	936	2	US-09-942-711-18	Sequence 20, Appl1	231	27	62.8	35	2	US-08-854-050-133	Sequence 133, App
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164	27	62.8	932	1	US-07-906-397A-2	Sequence 2, Appl1	237	27	62.8	35	2	US-08-974-549A-251	Sequence 251, App
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#### SUMMARIES

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## OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:04 ; Search time 8.77551 Seconds  
(without alignments)  
48.418 Million cell updates/sec

Title: US-10-067-484-5  
Perfect score: 43  
Sequence: 1 PYATEVXDXD 10

Scoring table: BLOSUM62  
Gap 10.0, Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 1000 summaries

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Published Applications AA.New:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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5	30	69.8	688	7	US-11-113-424-48
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7	30	69.8	688	7	US-11-040-218-25
8	30	69.8	688	7	US-11-040-218-27
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11	29	67.4	209	6	US-10-194-487-470
12	29	67.4	209	6	US-10-195-883-470
13	29	67.4	209	6	US-10-195-888-470
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15	29	67.4	326	6	US-10-226-486-29
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18	29	67.4	402	7	US-11-079-463-6274
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21	29	67.4	877	7	US-11-087-099-7068
22	28	65.1	104	6	US-10-467-657-7314
23	28	65.1	214	6	US-11-079-463-8122
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83	26	60.5	42	7	US-11-207-078-96	Sequence 96, Ap
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85	26	60.5	47	7	US-11-207-078-42	Sequence 42, Ap
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93	26	60.5	157	7	US-11-207-078-226	Sequence 226, Ap
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140	26	60.5	460	7	US-11-096-568A-8102	Sequence 8102, Ap	213	25	58.1	112	7	US-11-096-568A-15517	Sequence 15517, A
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147	26	60.5	480	7	US-11-188-298-1665	Sequence 1665, Ap	220	25	58.1	196	7	US-11-096-568A-23392	Sequence 23392, Ap
148	26	60.5	480	7	US-11-188-298-9166	Sequence 9166, Ap	221	25	58.1	196	7	US-11-096-568A-22390	Sequence 22390, A
149	26	60.5	490	7	US-11-188-298-6418	Sequence 6418, Ap	222	25	58.1	197	7	US-11-096-568A-10134	Sequence 10134, A
150	26	60.5	501	7	US-11-188-298-22165	Sequence 22165, A	223	25	58.1	214	7	US-11-096-568A-2391	Sequence 2391, Ap
151	26	60.5	501	7	US-11-188-298-19312	Sequence 19312, A	224	25	58.1	229	7	US-11-096-568A-10133	Sequence 10133, A
152	26	60.5	502	7	US-11-282-000-14	Sequence 14, Appl	225	25	58.1	240	7	US-11-079-463-5815	Sequence 5815, Ap
153	26	60.5	505	7	US-11-132-142-8	Sequence 8, Appl	226	25	58.1	245	6	US-10-511-538-227	Sequence 227, Appl
154	26	60.5	515	7	US-11-188-298-15437	Sequence 15437, A	227	25	58.1	247	7	US-11-000-440-399	Sequence 399, Appl
155	26	60.5	515	7	US-11-188-298-6418	Sequence 6418, Ap	228	25	58.1	247	7	US-11-096-568A-5686	Sequence 5686, Ap
156	26	60.5	516	7	US-11-188-298-11340	Sequence 11340, Ap	229	25	58.1	249	7	US-11-096-568A-2390	Sequence 2390, Ap
157	26	60.5	528	7	US-11-087-099-6670	Sequence 6670, Ap	230	25	58.1	249	7	US-11-096-568A-2393	Sequence 2393, Ap
158	26	60.5	539	7	US-11-188-298-13310	Sequence 13310, A	231	25	58.1	252	6	US-10-506-454-930	Sequence 930, Appl
159	26	60.5	550	7	US-11-052-554A-200	Sequence 200, App	232	25	58.1	258	7	US-11-090-463-871	Sequence 871, App
160	26	60.5	574	7	US-11-188-298-553	Sequence 523, App	233	25	58.1	275	7	US-11-096-568A-22436	Sequence 22436, A
161	26	60.5	589	7	US-11-188-298-10153	Sequence 10153, A	234	25	58.1	293	7	US-11-188-298-2617	Sequence 2617, Ap
162	26	60.5	606	7	US-11-079-463-10153	Sequence 4068, Ap	235	25	58.1	304	7	US-11-096-568A-25549	Sequence 25549, A
163	26	60.5	623	7	US-11-087-099-495	Sequence 495, App	236	25	58.1	306	7	US-11-072-512-3899	Sequence 3899, Ap
164	26	60.5	682	7	US-11-096-568A-30650	Sequence 30650, A	237	25	58.1	310	7	US-11-096-568A-18870	Sequence 18870, Ap
165	26	60.5	682	7	US-11-096-568A-14747	Sequence 14747, A	238	25	58.1	310	7	US-11-188-298-11569	Sequence 11569, A
166	26	60.5	687	7	US-11-096-568A-9967	Sequence 9967, Ap	239	25	58.1	314	7	US-11-188-298-11569	Sequence 18869, A
167	26	60.5	687	7	US-11-113-424-45	Sequence 45, Appl	240	25	58.1	314	7	US-11-188-298-18377	Sequence 18377, A
168	26	60.5	692	7	US-11-079-463-7997	Sequence 7997, Ap	241	25	58.1	322	6	US-10-194-487-172	Sequence 172, App
169	26	60.5	732	7	US-11-096-568A-6966	Sequence 6966, Ap	242	25	58.1	322	6	US-10-194-487-172	Sequence 172, App
170	26	60.5	737	7	US-11-152-366-28	Sequence 28, Appl	243	25	58.1	322	6	US-10-194-487-172	Sequence 172, App
171	26	60.5	737	7	US-11-152-366-28	Sequence 28, Appl	244	25	58.1	322	6	US-10-194-487-172	Sequence 172, App